

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 14, 2000, 10:30:22 ; Search time 38.96 Seconds
(without alignments)
517.680 Million cell updates/sec

Title: US-09-166-298-26_COPY_1_216
Sequence: 1 ISYSDPDYDSCFKISLR.....SPLKCTLLPPGQESSESASA 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPTRMBL_14:*
2: SP_archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_human:*
6: SP_invertebrate:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phase:*
10: SP_plant:*
11: SP_protent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1123	98.2	239	4	Q15467
2	515	45.0	513	11	Q35664
3	515	45.0	513	11	Q35238
4	510	44.6	247	11	Q35663
5	506	44.2	248	11	Q35983
6	233	20.4	508	13	Q9PVK0
7	229	20.0	508	13	Q9YHV9
8	112	9.8	553	4	Q9UHF4
9	89.5	7.8	897	4	Q08866
10	89	7.8	300	5	Q9XXK0
11	89	7.8	635	5	Q96151
12	87.5	7.6	445	3	Q9UVG2
13	86	7.5	989	10	Q9ZU00
14	85.5	7.5	266	5	Q9XUM9
15	85.5	7.4	318	7	Q19477
16	84.5	7.4	349	11	Q61190
17	83.5	7.3	479	12	Q9PKS1
18	83.5	7.3	1544	5	Q19194
19	83	7.3	429	2	Q87530

20	83	7.3	562	1	Q9U210
21	82.5	7.2	336	2	P74721
22	82.5	7.2	525	5	Q19893
23	82	7.2	310	2	Q47735
24	82	7.2	478	12	Q86632
25	82	7.2	1579	5	Q9VSR6
26	82	7.2	1904	11	Q64699
27	81.5	7.1	358	8	Q32302
28	81.5	7.1	388	2	Q9RM90
29	81.5	7.1	1004	5	Q94427
30	81	7.1	522	5	Q77387
31	80.5	7.0	253	5	Q94808
32	80.5	7.0	722	5	Q96243
33	80	7.0	245	2	P70959
34	79.5	6.9	489	12	P88988
35	79.5	6.9	583	12	Q9QAI4
36	79.5	6.9	1306	12	Q9YVU0
37	79	6.9	37	8	Q20065
38	79	6.9	454	2	Q51555
39	79	6.9	553	5	Q44561
40	79	6.9	611	13	Q9PRH9
41	79	6.9	658	5	Q9TZD0
42	79	6.9	2302	11	Q88488
43	78.5	6.9	123	2	Q51763
44	78.5	6.9	341	13	Q9YEC8
45	78.5	6.9	607	11	Q35360

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	239 AA.
Q15467	Q15467	Q15467		
AC	Q15467	Q15467		
DT	01-NOV-1996	(TREMURel. 01, Created)		
DT	01-NOV-1996	(TREMURel. 01, Last sequence update)		
DT	01-JUN-2000	(TREMURel. 14, Last annotation update)		
DE	SOLUBLE IFN ALPHA/BETA RECEPTOR PRECURSOR.			
GN	IFNABR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
NC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=BLOOD:			
RX	MEDLINE: 95279874.			
RA	NOVICK D., Cohen B., Tal N., Rubinstein M.;			
RT	"Soluble and membrane-anchored forms of the human IFN-alpha/Beta receptor."			
RL	J. Leukoc. Biol. 57:712-718(1995).			
CC	-I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
DR	EMBL: X89814; CAA61940.1; -.			
DR	INTERPRO: IPR000282; -.			
KW	Receptor; Signal.			
FT	SIGNAL.			
FT	CHAIN 27 239	POTENTIAL.		
SQ	SEQUENCE 239 AA: 27336 MW: 138DC54AA1CIA1A2 CRC64;	SOLUBLE IFN ALPHA/BETA RECEPTOR.		
Query Match	98.2%;	Score 1123;	DB 4;	Length 239;
Best Local Similarity	100.0%;	Pred. No. 1.5e-91;		
Matches 211;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ISYSDPDYDSCFKISLRNFRSLISWELKNHSIVPHNYLLTYIMKRPEDLKVVKKCA	60	
DB	27	ISYSDPDYDSCFKISLRNFRSLISWELKNHSIVPHNYLLTYIMKRPEDLKVVKKCA	86	
QY	61	NTTRSFCDLTDEMRSTHAAVYVLEGFSGNTTIFSCSHNFALIDMSPEPFELIVGFTN	120	
DB	87	NTTRSFCDLTDEMRSTHAAVYVLEGFSGNTTIFSCSHNFALIDMSPEPFELIVGFTN	146	
QY	121	HINWVKRPSIVEELQFDLSLIVIEQSEGIYKKHKPEIKGNMSGNTYIIIDKLIPTNY	180	

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DB 147 HINMVFPSTVEEELQFDLSLVEESEGIVKKHKEIKGNMNGFTYIDKLIPNTMY 206
OY 181 CAVYLEHSDQAVIKSPKCTLLPQGESE 211
DB 207 CAVYLEHSDQAVIKSPKCTLLPQGESE 237

RESULT 2
O35664 PRELIMINARY; PRT; 513 AA.
AC 035664;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE TYPE I INTERFERON RECEPTOR SUBUNIT PRECURSOR.
GN IFNAR2 OR IFNAR2C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57 BLACK/6; TISSUE=BRAIN.
RX MEDLINE: 97464076.
RA Kim S.H., Cohen B., Novick D., Rubinstein M.;
RT "Mammalian type I interferon receptors consists of two subunits:
RT IFNAR1 and IFNAR2."
RL Gene 196:279-286(1997).
DR EMBL: Y09865; CAA70992.1; -.
DR MGD; MGI:1098243; Ifnar2.
DR INTERPRO: IPR000282; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 513 AA: 56568 MW: 601BPECEFA8CB73 CRC64;
POTENTIAL.
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Query Match 45.0%; Score 515; DB 11; Length 513;
Best Local Similarity 47.7%; Pred. No. 1.5e-37;
Matches 102; Conservative 46; Mismatches 56; Indels 10; Gaps 5;

OY 8 YTDSCFTFKISLRNFRSLSWELKNHSIVPTHYTLTYINSKPPDLKVVNKCANTTSFC 67
DB 34 YPDEPCTINITIRNSRLILSWELKNKSGPPANYTLWTVMSKDNLTWKVNCSPOTKSSC 93
OY 68 DLTDEMSTHEAY-VTVLEFGSGNTLFCSHNFWLAIDMSFEPPEPEIYGFTHINVMV 126
DB 94 DVTDKMLEGMSYVAIVYHKGDLTYCRCS-DYIVANAPLEPPEPEIYGFTHINVTM 152
OY 127 KFP----SIVEELQFDLSLVEESEGIVKKHKEIKGNMNGFTYIDKLIPNTMYCV 182
DB 153 EFPVTSKIIOEKMKTPFVKEIGDSVKKHKEPKV-NNVTGNFTVLRDLPLKTNVCV 211
OY 183 SVYLEHSDQAVIKSPKCTLLPQGESESA 216
DB 212 SLVF--DDPAIKSPKCTVLPQGESESA 242

RESULT 3
O35238 PRELIMINARY; PRT; 513 AA.
AC 035238;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE TYPE I INTERFERON RECEPTOR PRECURSOR.
GN IFNAR2 OR IFNAR2C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97442458.
RA Owczarek C.M., Hwang S.Y., Holland K.A., Gulluyan L.M., Tavarina M.,
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RA Weaver B., Reich N.C., Kola I., Hertzog P.J.;
RT "Cloning and characterization of soluble and transmembrane isoforms of
RT a novel component of the murine type I interferon receptor, IFNAR 2."
RL J. Biol. Chem. 272:23865-23870(1997).
DR EMBL: AF013374; AAC53351.1; -.
DR MGD; MGI:1098243; Ifnar2.
DR INTERPRO: IPR000282; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 513 AA: 56623 MW: 602FC47D057EC372 CRC64;
POTENTIAL.
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```
Query Match 45.0%; Score 515; DB 11; Length 513;
Best Local Similarity 47.7%; Pred. No. 1.5e-37;
Matches 102; Conservative 46; Mismatches 56; Indels 10; Gaps 5;

OY 8 YTDSCFTFKISLRNFRSLSWELKNHSIVPTHYTLTYINSKPPDLKVVNKCANTTSFC 67
DB 34 YPDEPCTINITIRNSRLILSWELKNKSGPPANYTLWTVMSKDNLTWKVNCSPOTKSSC 93
OY 68 DLTDEMSTHEAY-VTVLEFGSGNTLFCSHNFWLAIDMSFEPPEPEIYGFTHINVMV 126
DB 94 DVTDKMLEGMSYVAIVYHKGDLTYCRCS-DYIVANAPLEPPEPEIYGFTHINVTM 152
OY 127 KFP----SIVEELQFDLSLVEESEGIVKKHKEIKGNMNGFTYIDKLIPNTMYCV 182
DB 153 EFPVTSKIIOEKMKTPFVKEIGDSVKKHKEPKV-NNVTGNFTVLRDLPLKTNVCV 211
OY 183 SVYLEHSDQAVIKSPKCTLLPQGESESA 216
DB 212 SLVF--DDPAIKSPKCTVLPQGESESA 242
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RESULT 4
O35663 PRELIMINARY; PRT; 247 AA.
AC 035663;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE SOLUBLE TYPE I INTERFERON RECEPTOR SUBUNIT PRECURSOR.
GN IFNAR2 OR IFNAR2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57 BLACK/6; TISSUE=BRAIN.
RX MEDLINE: 97464076.
RA Kim S.H., Cohen B., Novick D., Rubinstein M.;
RT "Mammalian type I interferon receptors consists of two subunits:
RT IFNAR1 and IFNAR2."
RL Gene 196:279-286(1997).
DR EMBL: Y09864; CAA70991.1; -.
DR MGD; MGI:1098243; Ifnar2.
DR INTERPRO: IPR000282; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 247 AA: 27609 MW: 4957A16710C2D2D1 CRC64;
POTENTIAL.
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Query Match 44.6%; Score 510; DB 11; Length 247;
Best Local Similarity 47.8%; Pred. No. 1.7e-37;
Matches 100; Conservative 45; Mismatches 54; Indels 10; Gaps 5;

OY 8 YTDSCFTFKISLRNFRSLSWELKNHSIVPTHYTLTYINSKPPDLKVVNKCANTTSFC 67
DB 34 YPDEPCTINITIRNSRLILSWELKNKSGPPANYTLWTVMSKDNLTWKVNCSPOTKSSC 93
OY 68 DLTDEMSTHEAY-VTVLEFGSGNTLFCSHNFWLAIDMSFEPPEPEIYGFTHINVMV 126
DB 94 DVTDKMLEGMSYVAIVYHKGDLTYCRCS-DYIVANAPLEPPEPEIYGFTHINVTM 152
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QY	127	KFP---	SVLEELQFDSLVIIEESSEIVKKHKEIGNSMGNSTTYIIDLKIPNTNCV	182
Db	153	FFPPTSTIIQEKMKTTTFVVIKEQIGDSVRKKHEKV	NNVTGNFTFYLRDLLPTNTNCV	211
QY	183	SVLEHSDQAVIKSPKCTLLPQGESE	211	
Db	212	SLVF---	DDDPAIKSPKCIVLQPGQFSE	237
RESULT	5			
ID	035983	PRELIMINARY;	PRT;	248 AA.
AC	035983;			
DT	01-JAN-1998	(TREMblrel. 05, Created)		
DT	01-JAN-1998	(TREMblrel. 05, last sequence update)		
DT	01-JUN-2000	(TREMblrel. 14, last annotation update)		
DE	TYPE I INTERFERON RECEPTOR SOLUBLE	ISOFORM PRECURSOR.		
GN	IFNAR2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 97442458.			
RA	Owczarek C.M., Hwang S.Y., Holland K.A., Gulluyan L.M., Tavaría M.,			
RT	Weaver B., Reich N.C., Kola I., Hertzog P.J.,			
RT	"Cloning and characterization of soluble and transmembrane isoforms of			
RT	a novel component of the murine type I interferon receptor, IFNAR 2.;"			
RL	J. Biol. Chem. 272:23865-23870(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Owczarek C.M., Hwang S.Y., Holland K.A., Gulluyan L.M., Tavaría M.,			
RA	Weaver B., Reich N., Kola I., Hertzog P.J.;			
RL	Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-C57 BLACK/6; TISSUE-BRAIN;			
RX	MEDLINE: 97464076.			
RA	Kim S.H., Cohen B., Novick D., Rubinstein M.;			
RT	"Mammalian type I interferon receptors consists of two subunits:			
RT	IFNAR1 and IFNAR2.;"			
RL	Gene 196:279-286(1997).			
DR	EMBL: AF0133486; AAC53352.1; -			
DR	EMBL: Y09813; CAA70943.1; -			
DR	MGD: MGI:1096243; Ifnar2.			
DR	INTERPRO: IPR000282; -			
KW	Signal.			
FT	SIGNAL			
FT	CHAIN	1	27	POTENTIAL.
FT		28	248	TYPE I INTERFERON RECEPTOR SOLUBLE
FT				ISOFORM.
SO	SEQUENCE	248 AA;	27755 MW;	47DD008193F7BC3C CRC64;

RESULT	6			
09PVK0				
ID	09PVK0	PRELIMINARY;	PRT;	508 AA.
AC	09PVK0;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2000 (TREMBLrel. 13, Last annotation update)			
DE	INTERFERON ALPHA/BETA RECEPTOR 2.			
GN	IFNAR2.			
OS	Gallus gallus (Chicken).			
OC	Archaeopta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archaeopta; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 99177346.			
RA	Rabouli J, Gardiner K, Monneron D, Uze G, Lutfalla G;			
RT	"Comparative genomic analysis of the Interferon/Interleukin-10			
RT	receptor gene cluster."			
RL	Genome Res. 9:242-250(1999).			
DR	EMBL; AF082667; AAD13677.1; ..			
DR	INTERPRO; IPR000282; -			
DR	INTERPRO; IPR001187; -			
DR	INTERPRO; IPR002048; -			
DR	PRINTS; PR00346; TISSUEFACTOR.			
DR	PROSITE; PS00018; EF_HAND, UNKNOWN_1.			
KW	Receptor.			
SO	SEQUENCE	508 AA;	57175 MW;	4C02D29D243E8C05 CRC64;

	Query Match	44.2%	Score 506:	DB 11:	Length 248:
	Best Local Similarity	47.4%	Pred. No. 3,8e-37:		
	Matches	100:	Conservative	45:	Mismatches 56: Indels 10: Gaps 5:
OY	8	YTDSECTKISLRNRSILSMELKNSIYPHTYLLITLMTSPEDLKYYKNCANNTTRSC	67		
		:			
Db	34	YRDECTINITNTRSLRLISLWELKNSGPRATYLMYVSDENLTYYKNCSDTTKSSC	93		
OY	68	DLTDEMRSTHEAY-VTVLEGFSGNTTLTSCSHNFALIDMSRPEPEFLVGTNNHNVAY	126		
		: : :			
Db	94	DVTDLKGMESMEYVAIVIHNRGDLTVCCS-DYIYAPAPARLEPPEFLVGTTHDINVTM	152		
OY	127	KRP----SLVESLQFDLSIVTEBQSEGVKHKHPKIGMSNGNTYIIDLIPNTNVY	182		
		: : : : : : : : :			
Db	153	ERRPYTSKIQLQKMTTPRVIVKEQIGDSYRKKNHKEYV-NNTYGNTEFLVRLDLPKNTNVY	211		
OY	183	SVYLESHDQAVIKSPKLCTLLRPQDSESA	213		
		: : :			
Db	212	SLYF---DDDPAIKSPKCTVLIQDPQDSGMA	239		

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Query Match      20.4%; Score 233; DB 13; Length 508;
Best Local Similarity 27.0%; Pred. No. 1,1e-12;
Matches 56; Conservative 46; Mismatches 81; Indels 30; Gaps

QY 1 ISYSPDYTDESCFEKISLNFNRSILSMELKNHSIVPHYHTLYLTIMSKPEDLVKNCA 60
Db 32 IPRPPD-----MIQMSNNFOHILSWRAHSDPTVPTVYEVLY---SSHSNMKIAQCS 82
QY 61 NTRSPCOLNDEMRSKTHNAVYTVLEGSGNTLTFSCSHNEFLALIDMSF-BPPEEIVGFT 119
Db 83 RIYQFPCMLHDDFOVYSDEYSAPVQSFEVG-TEVNSLSILYSPLESTFLPPEPRLSSCV 149
QY 120 NHINWAKFPSI-----VEEELQFDLSLVIQESGCIYVKKHKPEIKGNMSGN 166
Db 142 HCINTITIKLPETHLRKNGKLLSLFDIYNKVVYEITL-----RTVGEEHKKSPKVTPEP 195
QY 167 FTYIIDKLIPTNTNCVSYLYLESHSDQAVIKPLKGC 201
Db 196 FSIVIEELYPNRKNCYSVMYATSLNKKSHIPSAKRC 230

RESULT 7
Q9YHV9 PRELIMINARY; PRT; 508 AA.
AC Q9YHV9 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 2.
GN IFNAR2.
OS Gallus gallus (Chicken)..
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RC [1]
RN SEQUENCE FROM N.A.
RP TISSUE=LIVER;
RC Rebolu J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
KT receptor gene cluster.";
RL Genome Res. 0:0-0(1999).
EMBL; AF082665; AAD13670.1; -.
OR

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DR HSSP: P13726; 1TFH.
 DR INTERPRO: IPR000282; -.
 DR INTERPRO: IPR001187; -.
 DR INTERPRO: IPR002048; -.
 DR PEAM: PE01108; Tissue.faci: 1.
 DR PRINTS: PR00346; TISSUEFACTOR.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
 DR Receptor.
 KW Receptor.
 SQ SEQUENCE 508 AA; 57049 MW; 5CE6DFED970DFB90 CRC64;

Query Match 20.0%; Score 229; DB 13; Length 508;
 Best Local Similarity 27.0%; Pred. No. 2,4e-12;
 Matches 58; Conservative 45; Mismatches 82; Indels 30; Gaps 6;

QY 1 ISYSDPDYDESCTFKISLNFPSRISLWELKNHSIVPTHTYLLTYLTKSKPEDLKVNCA 60
 DB 32 IPREPD-----NLQMTSNFQHILSMRAHSDPTVPTTYRVLY---SSHSNMKIKAKCS 82
 QY 61 NTRSFCDLTDENRSTHEAVTVLEGFSGNTLFCSCSHNFWLAIDMSF-EPPFEIIVGFT 119
 DB 83 RIQVPCNLTDDEFOVVSDEYSAFQSFVG-TEVFNSSLHFSPLETFILGPPPEFNLSGV 141
 QY 120 NHTNWWKPPSI-----VEELQFPLSLVIEQSGIYKKHPELKGNSGN 166
 DB 142 HCNITIKLPPTHLRKNKILLSFDIYNKYNVEITL-----RTVGEHRKSPKYTEEP 195
 QY 167 FTYIIDLKLPNTNYCVSVYLEHSEDAVAKSPKLC 201
 DB 196 FSIYIEELVPRNRYCVSVMTATSLNKHSTPSAMKC 230

RESULT 8
 Q9UHF4 PRELIMINARY; PRT; 553 AA.
 AC Q9UHF4:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CLASS II CYTOKINE RECEPTOR ZCYTOR7.
 GN ZCYTOR7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN 11
 RP SEQUENCE FROM N.A.
 RA Lok S., Kho C., Jelmberg A., Adams R., Whitmore T., Farrah T.,
 O'Hara P.;
 RT "Homo sapiens cytokine receptor homolog.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN 12
 RP SEQUENCE FROM N.A.
 RA Prenen S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
 Martinez T., Hoffman R., O'Hara P.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF184971; AAF01320.1; -.
 DR INTERPRO: IPR000282; -.
 KW Receptor.
 SQ SEQUENCE 553 AA; 62533 MW; 7C23C8543B114659 CRC64;

Query Match 9.8%; Score 112; DB 4; Length 553;
 Best Local Similarity 23.7%; Pred. No. 0.054;
 Matches 42; Conservative 33; Mismatches 82; Indels 20; Gaps 7;

QY 21 NTRSIISWE-----LKNHSIVPTHTYLLTYLTKSKPEDLKVNKANTRSFCDLTDENRS- 75
 DB 49 NKNVNLQMTPEPLOG---VKYTVQVYFYGQKKWLN-KSECRNINRTKFCDSLAEISDV 104
 QY 76 THEAVTVLEGFSGNTLFCSCSHNFWLAIDMSFEPPEFELVGTNHNINWWKPPSIVEEE 135
 DB 105 EHOYIAKVAIKWGTCKSKMAESGRFPLETOIGPPEVALTTDEKISIVLTAPEKWKRN 164

QY 136 LQFDSLVLIEQSGEIGYKKHKPEIKGNMSG-----NETYIIDKLPNTNYCVSV 184
 DB 165 PE-DLPSVMOQIYSNLN--KYNVSVLNTKSNRTWSQCVTNTHTLVLTWLEPPTLYCAVH 218

RESULT 9
 Q08886 PRELIMINARY; PRT; 897 AA.
 AC Q08886:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
 DE CHROMOSOME XV READING FRAME ORF YOR371C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN 11
 RP SEQUENCE FROM N.A.
 RA Delius H., Hebling U., Hofmann B.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN 12
 RP SEQUENCE FROM N.A.
 RA MIPS:
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z75279; CAA99702.1; -.
 SQ SEQUENCE 897 AA; 100939 MW; DEA78275A515BC29 CRC64;

Query Match 7.8%; Score 89.5; DB 3; Length 897;
 Best Local Similarity 21.2%; Pred. No. 9.5;
 Matches 58; Conservative 28; Mismatches 68; Indels 119; Gaps 14;

QY 3 YDSPDYDESCTFKISLNFPSRISLWELKNHSIVPTHTYLLTYLTKSKPEDLKVNCA 60
 DB 155 YDFEDNTDDCNKACGAFYSSERLEILRSRTISIFKYYKKLLVYDLRDSVLRHNL 214
 QY 36 ----VPTHTYLLTYLTKSKPE-----DLKVNKANTRSFCDLTDENRSTH 77
 DB 215 WMDMTRFRFFFLVSSSKPEDVRLTPITPFSSELDIFKN--KTCPLFINGTD---CVP 269
 QY 78 EAVTVLEGFSGNTLFCSCSHNFWLAIDMSFEPPEFELVGTNHNINWWKPPSIVEEEO 137
 DB 270 RSYDT-----FSGSSVIAISIF-----SEYKLPISLYHCSV-----ELN 302
 QY 138 FDSLVLIEQSGEIGYKKHKPEIKGNMSGFTYIIOK 173
 DB 303 DQEFIV-----GGLMACHRYDEEAPDLKDYVGICKINLPPILPELINNPS----- 348
 QY 174 LIPNTN-YCVSV--YLEHSEDAVAKSPKLC 202
 DB 349 MIPNPLVCFSLTSSRLTRPDISGYIPLPLVCF 361

RESULT 10
 Q9XXKO PRELIMINARY; PRT; 300 AA.
 AC Q9XXKO:
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE T05G11.2 PROTEIN.
 GN T05G11.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peioderinae; Caenorhabditis.
 RN 11
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 94150718.
 RA Wall M.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN 12

RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA Wilson R., Ainscough R., Anderson K., Baynes C., Belts M.,
RA Bonfield J., Button J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Keshaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken R., Roopra A., Saunders R., Showkneen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Stilson J.,
RA Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson S., Weinstock L., Wilkinson-Sprat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RT Nature 368:32-38 (1994).
RL EMBL: AL023816; CAA19430.1; -.
DR INTERPRO: IPR002892; -.
DR PRAM: PF01838; DUF40; 1.
SO SEQUENCE 300 AA; 34568 MW; 8BF23B2AF2B35B5A CRC64;

[illegible]

RESULT	11	
096151		
ID	096151	PRELIMINARY; PRT; 635 AA.
AC	096151;	
DT	01-MAY-1999 (TREMBLrel, 10, Created)	
DT	01-MAY-1999 (TREMBLrel, 10, Last sequence update)	
DT	01-MAY-1999 (TREMBLrel, 10, Last annotation update)	
DE	HYPOTHETICAL 76.4 KDA PROTEIN.	
GN	PFB0250W.	
OS	Plasmodium falciparum.	
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 99021743.	
RA	Gardner M.J., Feltelin H., Carnuci D.J., Cummings L.M., Aravind L.,	
RA	Koonin E.V., Shallow S., Mason T., Yu K., Fujii C., Pederson J.,	
RA	Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pereira M.,	
RA	Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,	
RA	Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;	
RT	"Chromosome 2 sequence of the human malaria parasite Plasmodium	
RT	falciparum.";	
RL	Science 282:1126-1132(1998).	
DR	EMBL; AE001382; AAC71839.1; .	
KM	Hypothetical protein.	
SO	SEQUENCE	635 AA; 76449 MW; DDB063DC15C15459 CRC64;

Query Match	7.8%	Score	89	DB	5	Length	635
Best local similarity	24.2%	Pred	No	6.8%			
Matches	40	Conservative	35	Mismatches	46	Indels	44
						Gaps	11

RESULT	12		
09UVG2			
ID	09UVG2.	PRELIMINARY:	PRT: 445 AA.
AC	09UVG2.		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)		
DE	ORITHTHINE DECARBOXYLASE.		
GN	ODC1.		
OS	Phaeosphaeria nodorum (Septoria nodorum).		
OC	Eukaryota; Fungi; Ascomycota; Dothideales; Phaeosphaeriaceae;		
OC	Phaeosphaeria.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-LAW 95;		
RA	Bailey A., Mueller E., Bowyer P.;		
RT	"Ornithine decarboxylase gene of Stagonospora (Septoria) "		
RL	Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AJ249387; CAB56523.1; -.		
DR	INTERPRO; IPR000183; -.		
DR	INTERPRO; IPR002433; -.		
DR	PFAM; PF00278; Orn_DAP_Arg_dec; 1.		
DR	PRINTS; PR01179; ODADCRBX1ASE.		
DR	PRINTS; PR01182; ORNDCRBX1ASE.		
DR	PROSITE; PS00878; ODR_DC_2.1; UNKNOWN_1.		
DR	PROSITE; PS00879; ODR_DC_2.2; UNKNOWN_1.		
SO	SEQUENCE 445 AA; 48937 MW; D59CA6642C75C00B CRC64;		

[illegible]

RESULT	13
09ZU00	
ID	09ZU00
AC	PRELIMINARY;
DT	PRT; 989 AA.
DT	01-MAY-1999 (TREMBlrel. 10, Created)
DT	01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT	01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE	CHP-RICH HYPOTHETICAL PROTEIN SIMILAR TO T10M13.16.
DE	T10M13.17.1.
CS	Arbidoposis thaliana (Mouse-ear cross).

us-09-166-298-26_copy_1_216.rspt

```

Db 106 AYDGDGFIVFDKDFLSMLANDVAHIIKRWANLH-----ELÖYÖK 147
QY 58 N-----CANTTRASCDFL-TDEMRSTHAYV--TVLESGFSCNTLFCSCNFWLAIDMSFE 109
Db 148 NMLEECCJAWLKRFLFEGSDALERTHEPVPVTKTEKFPBITTLFCRAHGFY----- 199
QY 110 PREEIYGFTHHINWVKRPSIYEEELDFDLSVIEGSGEYKHKHKLKGMV-SGNFT 168
Db 200 PPE-----ISMWKNGEIVQ--EVDYGVLPSCDGT 230
QY 169 Y---IDKLIPNTNYCVSVYLEHSDQAVIKSP 198
Db 231 YQMWVSVDLPQTKDITSCHAEHSGDLMILEAP 263

```

Search completed: December 14, 2000, 10:30:25
Job time: 218 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2000, 10:28:19 ; Search time 27.57 seconds
(without alignments)
497.186 Million cell updates/sec

Title: US-09-166-298-26_COPY_1_216
Perfect score: 1144
Sequence: 1 ISYSPDYTDESCTFKISLR.....SPLKCTLLPQGESSESASSA 216

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR.65:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1144	100.0	331	2 A54295	interferon alpha/b
2	1144	100.0	331	2 S59501	interferon recepto
3	1144	100.0	515	2 S59502	interferon recepto
4	1140	99.7	515	2 I39073	interferon alpha-b
5	129	11.3	292	1 KFB03	tissue factor prec
6	110.5	9.7	295	1 KFRH3	tissue factor prec
7	107.5	9.4	292	1 KFRB3	tissue factor prec
8	99	8.7	1501	2 S57198	multidrug resistan
9	97	8.5	294	1 KFRM3	tissue factor prec
10	95	8.3	752	2 S51866	HPRI protein - yea
11	94	8.2	557	2 A32694	interferon alpha/b
12	90.5	7.9	325	2 A47003	cytokine receptor
13	90.5	7.9	337	2 I38500	interferon gamma r
14	89.5	7.8	273	2 G01418	cytokine receptor
15	89.5	7.8	897	2 S67283	hypothetical prote
16	89	7.8	300	2 T24547	hypothetical prote
17	89	7.8	635	2 A71620	hypothetical prote
18	88	7.7	1238	2 S68700	HPRT beta-like tyr
19	86.5	7.6	846	2 JN0324	lysine aminopeptid
20	86.5	7.6	997	2 S26426	type IV site-speci
21	86	7.5	989	2 T01519	hypothetical prote
22	86	7.5	1747	1 A45974	collagen alpha 1(X
23	86	7.5	1857	2 S31212	collagen alpha 1(X
24	86	7.5	1888	2 S78476	collagen alpha 1(X
25	85.5	7.5	266	2 T26068	hypothetical prote
26	85	7.4	560	2 S27387	interferon alpha r
27	84.5	7.3	988	1 S23157	membrane alanyl am
28	84	7.3	988	1 DJV2FP	DNA-directed DNA p
29	83.5	7.3	349	2 JC6311	interferon recepto

30	83.5	7.3	1544	2 T29482	hypothetical prote
31	83	7.3	562	2 G75044	acetolactate synth
32	83	7.3	1907	2 S50893	protein-tyrosine-p
33	82.5	7.2	336	1 S76928	probable aryl alco
34	82.5	7.2	525	2 T21527	hypothetical prote
35	82	7.2	298	2 A32872	myogenic factor CM
36	82	7.2	298	2 A33783	transcription regu
37	82	7.2	478	2 JQ2034	RNA-directed RNA p
38	82	7.2	489	2 A31555	interferon gamma r
39	81.5	7.1	479	2 T47415	transporter-like p
40	81.5	7.1	1004	2 T31665	hypothetical prote
41	81.5	7.1	1086	2 B71667	isoleucine--tRNA l
42	81	7.1	493	2 A33809	cartilage matrix p
43	81	7.1	522	2 T18504	hypothetical prote
44	81	7.1	590	2 A45283	interferon alpha/b
45	81	7.1	662	2 T20343	hypothetical prote

ALIGNMENTS

RESULT 1
A54295
Interferon alpha/beta receptor precursor - human
C:Species: Homo sapiens (man)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999
C:Accession: A54295
R:Novick, D.; Cohen, B.; Rubinstein, M.
Cell 77, 391-400, 1994
A>Title: The human Interferon alpha/Beta receptor: characterization and molecular clo
A:Reference number: A54295; MUID:94236684
A:Accession: A54295
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-331 <NOV>
A:Cross-references: GB:X77722; NID:9488363; PIDN:CA454785.1; PID:9488364
C:Keywords: cytokine receptor

Query Match 100.0%; Score 1144; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 6.4e-93;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISYSPDYTDESCTFKISLRNFRSILSMELKNHSIVPTHTLYTINSKPEDLKVNCA 60
|||||
Db 27 ISYSPDYTDESCTFKISLRNFRSILSMELKNHSIVPTHTLYTINSKPEDLKVNCA 86
QY 61 NTRSFCDLDEWMSRTHDAYVTVLEGFSGNTTLFSCSHNFWLAIDMSFEPPEFIVGFTN 120
|||||
Db 87 NTRSFCDLDEWMSRTHDAYVTVLEGFSGNTTLFSCSHNFWLAIDMSFEPPEFIVGFTN 146
QY 121 HINWVWFRPSIVEEELQFDLSLTVIEOSEGVKKHKHPRKKNMNGNTYIIDKLIPMTNY 180
|||||
Db 147 HINWVWFRPSIVEEELQFDLSLTVIEOSEGVKKHKHPRKKNMNGNTYIIDKLIPMTNY 206
QY 181 CVSVYLEHSDQAVIKSPKCTLLPQGESSESASSA 216
|||||
Db 207 CVSVYLEHSDQAVIKSPKCTLLPQGESSESASSA 242

RESULT 2
S59501
Interferon receptor JFNAR 2-1 - human
C:Species: Homo sapiens (man)
C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S59501
R:Lutfulalla, G.; Holland, S.J.; Chatalo, E.; Monneron, D.; Reboul, J.; Rogers, N.C.; Sm
EMBO J. 14, 5100-5108, 1995
A>Title: Mutant USA cells are complemented by an Interferon-alpha-beta receptor subun
A:Reference number: S59501; MUID:96067138
A:Accession: S59501
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: mRNA

A;Residues: 1-331 <LUT>
C;Keywords: alternative splicing; cytokine receptor

Query Match	100.0%;	Score 1144;	DB 2;	Length 331;
Best Local Similarity	100.0%;	Pred. No. 6.4e-93;		
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ISYDPOYTDSCAPKISLRNFRSTLSWELKNHSTVPHNYHTLLTYIMSKPEDLKVKKCA	60
Db	27	ISYDPPDTDESCPIKISLRNFRSTLSWELKNHSTVPHNYHTLLTYIMSKPEDLKVKKCA	86
QY	61	NTTRSCDLTDEMRSTHEAYVYVLEGFSGNTLLFSCSHNFWLAIDMSEPEPELIVGFTN	120
Db	87	NTTRSCDLTDEMRSTHEAYVYVLEGFSGNTLLFSCSHNFWLAIDMSEPEPELIVGFTN	146
QY	121	HINWVKRPSVIEEELQFDLSLIVIEGSEGIVKKHKPEIKGMGSGNTFYIIDKLIPNTNY	180
Db	147	HINWVKRPSVIEEELQFDLSLIVIEGSEGIVKKHKPEIKGMGSGNTFYIIDKLIPNTNY	206
QY	181	CVSYVLEHSDRAVYIKSPKCTLLPPGOESBSAESA	216
Db	207	CVSYVLEHSDRAVYIKSPKCTLLPPGOESBSAESA	242

```

RESULT      3
S59502
Interferon receptor JFNAR 2-2 - human
C:Species: Homo sapiens (man)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S59502
R:Luttfalla, G.; Holland, S.J.; Ciardo, E.; Monneron, D.; Reboul, J.; Rogers, N.C.; Smittick
EMBO J. 14, 5100-5108, 1995
A:Title: Mutant USA cells are complemented by an interferon-alpha-beta receptor subunit
A:Reference number: S59501; MUID:96067138
A:Accession: S59502
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tree
A:Molecule type: mRNA
A:Residues: 1-515 <LUT>
A:Keywords: alternative splicing; cytokine receptor

```

Query Match	100.0%;	Score 1144;	DB 2;	Length 515;
Best Local Similarity	100.0%;	Pred. No. 1.1e-92;		
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ISYSPDYTDSCFCKISLRNFRSLISWELKNHSTVPHHTLLTYIMSKPELKVKKCA	60
Db	27	ISYSPDYTDSCFCKISLRNFRSLISWELKNHSTVPHHTLLTYIMSKPELKVKKCA	86
QY	61	NTTTSFCOLJDEMRSTHAEAYVTVLEGFSGNTTLFSCSNFMIAIDMSFPEFETVGFN	120
Db	87	NTTTSFCOLJDEMRSTHAEAYVTVLEGFSGNTTLFSCSNFMIAIDMSFPEFETVGFN	146
QY	121	HIINWAKRPPSYEEELQFDLSLVIEQSEGIVKKHKPEIKGMMSGNFYYIIDKLIPNTNY	180
Db	147	HIINWAKRPPSYEEELQFDLSLVIEQSEGIVKKHKPEIKGMMSGNFYYIIDKLIPNTNY	206
QY	181	CVSVYLEHSDQAVIKSPILKCTLLPQGQESGSAESA	216
Db	207	CVSVYLEHSDQAVIKSPILKCTLLPQGQESGSAESA	242

RESULT 4
I39073
Interferon alpha-beta receptor, beta subunit long form - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C:Accession: I39073
R:Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.; Pitha, P.; Colamonici, J. Biol. Chem. 270, 21606-21611, 1995
A:Title: Cloning and expression of a long form of the beta subunit of the interferon alpha-
:Reference number: I39073; MUID:95394915

A:Accession: I39073
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-515 <RES>
A:Cross-references: EMBL:U29584; NID:g993040; PID:nAAC50202.1; PID:g993040
A:Keywords: cytokine receptor

Query Match	99.78;	Score 1140;	DB 2;	Length 515;
Best Local Similarity	99.58;	Pred. No. 2.6e-92;		
Matches 215; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	ISYSPDYTDSSCFKJISLNFRSILSMELKNISIVPTHLLTYLTMSKREDLKVKNNA	60
Db	27	ISYSPDYTDSSCFKJISLNFRSILSMELKNISIVPTHLLTYLTMSKREDLKVKNNA	86
Qy	61	MTTRSFCDLTDEMRSTHEAVYTVLEGFSGMNTLPSCSHNFWLAIDMSFEPPEFIEIGFTN	120
Db	87	MTTRSFCDLTDEMRSTHEAVYTVLEGFSGMNTLPSCSHNFWLAIDMSFEPPEFIEIGFTN	146
Qy	121	HINWVKRPSIVEEELQFDLSLVIEEGSEGIYVKKHKRPEIKGNMSGNTYIIIDLIPNTNY	180
Db	147	HINWVKRPSIVEEELQFDLSLVIEEGSEGIYVKKHKRPEIKGNMSGNTYIIIDLIPNTNY	206
Qy	181	CVSYVLEHSDQAVIKSPKLTLLPPQDESSASASA	216
Db	207	CVSYVLEHSDQAVIKSPKLTLLPPQDESSASASA	242

RESULT 5
KFB03
tissue factor precursor - bovine
N:Alternate names: coagulation factor III
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1992
C:Accession: J01319
R:Itakayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
A:Title: cDNA and amino acid sequences of bovine tissue factor.
A:Reference number: J01319; WUID:92109720

A:Residues: 1-292 <TAK>
A:Cross-references: GB:SF4147; NID:g241438; PIDN:ABB20755.1; PID:g241439
A:Experimental source: adrenal gland
A:Note: part of this sequence, including the amino end of the mature protein, was com
A:Comment: Tissue factor is an integral membrane glycoprotein that serves as a recep
C:Comment: Expression of tissue factor can be induced in a variety of tissues by cellu
C:Superfamily: tissue factor
C:Keywords: blood coagulation; glycoprotein; lipoprotein; thiol-ester bond; transmembr
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-292/Product: tissue factor #status experimental <KAT>
F:36-248/Domain: extracellular #status predicted <EXT>
F:249-271/Domain: transmembrane #status predicted <TM>
F:272-292/Domain: intracellular #status predicted <INT>
F:443-153,181/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:81-89,215-238/Disulfide bonds: #status predicted
F:118,124/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match	11.3%;	Score 129;	DB 1;	Length 292;
Best Local Similarity	23.0%;	Pred. No. 0.00058;		
Matches	53;	Conservative	38;	Mismatches 77;
				Indels 62;
				Gaps 11

```

0y 9 TDESCFETISLR--NFRSLIMELK--NHSIVPHVLTLYIMSKPEDLKVKVNCAMTFR 64
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 TDVVAVYAIITKRSINFEKILEMEPRINH-----VYIVQISPRGKNKNCFFYTN 86
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0y 65 SFCDLTDE--MSTHEAVYVYIEGFSGNTLTSCSHNEFLAIDMSFEPPEEIVGFTNHIN 122
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 87 TCDCTDDEIVNRRVYIARLYSPADS-----SSIVPEPFTNSPEFTYLE 134
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```



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Oy 21 NFRSILSMELKNHSIVPTHYLLTYITMSKPEDLKVVKNCANTRSFCDLTDE----WRST 76
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 48 NFKTILMEPKSIDHY---YTV---QISTRLNNK---SKCFLFAETBCDILDEIVKDVGC 100
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 77 HEKYYIVLEGSGNTTLFSCSNHFWLAIDMSFPPPEIYGVFNHINWVKFESYIE-EE 135
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 101 YKARVLYSTPARNCNTTGF-----PEEPFRNSPEFPYDITNMGOPTIOSFED 148
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 136 LQFDLSLVIEEOSEGIVKKHKRPET-----KGNMGSNFT-----YIT 171
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 149 VGRKLVAVYQD-AKTLVRKRGFTLSLRVFGKDLNTLYWRASSSGKKTATNTNEFLI 207
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 172 DKLIPTNVCVSYLHSDQAVI-----KSP---LKCTLLPQGESE 211
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 208 D-VDKGENCFSV-----QAVIPSRKRKRQRPESULTECTSREGGRARE 249
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
multidrug resistance protein CDRI - yeast (Candida albicans)
C:Species: Candida albicans
C>Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Sep-1999
C:Accession: S57198; S42025
R:Praad, R.; de Weertfosse, P.; Goffeau, A.; Balzi, E.
Curr. Genet. 27, 320-329, 1995
A>Title: Molecular cloning and characterization of a novel gene of Candida albicans, CDR
A:Reference number: S57198; MUID:95339406
A:Accession: S57198
A:Molecule type: DNA
A:Residues: 1-1501 <PRA>
A:Cross-References: EMBL:X77589; NID:g454276; PIDN:CAA54692.1; PID:g454277
C:Genetics:
A:Gene: CDR1
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C:Keywords: ATP; P-loop; transmembrane protein
F:170-380/Domain: ATP-binding cassette homology <ABC1>
F:878-1078/Domain: ATP-binding cassette homology <ABC2>
F:895-902/Region: nucleotide-binding motif A (P-loop)

Query Match      8.7%; Score 99; DB 2; Length 1501;
Best Local Similarity 25.4%; Pred. No. 2.2;
Matches 49; Conservative 17; Mismatches 63; Indels 64; Gaps 11;

Oy 8 YNDESCTFRISLNFPSIISLMELKNHSIVPTHYLLTYITMSKPEDLKVVKNCANTRSFC 67
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 841 FTFKSGTGSVDPPENKEIFFWR-----DLTYQVKIKED-----RVIL 878
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 68 DLTDERRSTHEAVYVLEGFSG--GNITLFSFSC-----SHNFWLAIDMS 107
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 879 DHVDCW--VKPQGITALMGASGAGKTTLLNCISERVYTGITDGERLVNCH---ALDSS 932
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 108 FEPPEEIGFTNHINWVKFPSIVFEELQFDLSLVIEQDSSEIVKKHKPEIKGMSGNF 167
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 933 FQ---RSIGYVQODVHLP-TSTVREALQFSAYL---RQSNKRSIKREKDDY-----V 977
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 168 TYIIDKLIPNTNY 180
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 978 DYVID-LLEKMTDY 989
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
KEMS3
tissue factor precursor - mouse
N:Alternate names: coagulation factor III
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C:Accession: A32318; A39046
R:Hartzell, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
Mol. Cell. Biol. 9, 2567-2573, 1989
A>Title: A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a protein hc
A:Reference number: A32318; MUID:89343974
A:Accession: A32318

```

```

A:Molecule type: mRNA
A:Residues: 1-294 <HAR>
A:Cross-References: GB:M57896; NID:g201924; PIDN:AAA0414.1; PID:g201925
R:Ramanathan, G.; Blatti, S.P.; Subramaniam, M.; Fass, D.N.; Mahle, N.J.; Getz, H.J.
J. Biol. Chem. 266, 496-501, 1991
A>Title: Cloning of murine tissue factor and regulation of gene expression by transfo
A:Reference number: A39046; MUID:91093171
A:Accession: A39046
A:Molecule type: mRNA
A:Residues: 1-25, '1', 27-294 <RAN>
A:Cross-References: GB:M57896; GB:J05713; NID:g201926; PIDN:AAA63400.1; PID:g201927
A>Note: 26-Tyr was also found
C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a recept
C:Comment: Expression of tissue factor can be induced in a variety of tissues by cert
C:Superfamily: tissue factor
C:Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembr
F:1-29/Domain: signal sequence #status predicted <SIC>
F:30-294/Product: tissue factor #status predicted <MNT>
F:30-251/Domain: extracellular #status predicted <EXT>
F:252-274/Domain: transmembrane #status predicted <TMN>
F:37,57,169,200/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:75-83, 218-241/Disulfide bonds: #status predicted
F:275/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match      8.5%; Score 97; DB 1; Length 294;
Best Local Similarity 25.8%; Pred. No. 0.37;
Matches 61; Conservative 26; Mismatches 71; Indels 78; Gaps 15;

Oy 21 NFRSILSMELKNHSIVPTHYLLTYITMSKPEDLKVVKNCANTRSFCDLTDE----NR 74
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 44 DFKTILEMQPK-----PTNYT--YTVQISDRSRNMKNKCFSTDTDECDDLDEIVKDVWT 95
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 75 STHEAVYTVL-----EG---FSGNTTLFSCSNHFWLAIDMSFEP---EPEIVGFT 119
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 96 -AEAAVLYSPRRNSVHGDDQLVHGEPPFTNAKFLPYRDTNLGQPYIQGFEDG--- 152
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 120 NHINWVKFP-SIVEELOF-----DLSLVIEEOSEGIVKKHKPEIKGMSGNFTY 169
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 153 RKLNVVVKOSLTVLRKNGFTLIRQVFGKDLGYIIYR-----KSSSTQKKTIN 200
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 170 IIDLIPNTN-----YCVSYLHSDQAVIKSPLKCTLLPQGESESAE 214
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 201 -----ITNTNFSIDVEEGVSYCFV-----QAMIFS-RKTNQNSPGSSTVCTE 243
      ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
S51866
HPRI protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YD9302.14; protein YDR138w
C:Species: Saccharomyces cerevisiae
C>Date: 05-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Mar-2000
C:Accession: S51866; A34781
R:Oliver, K.; Harris, D.
submitted to the EMBL Data Library, February 1995
A:Reference number: S51853
A:Accession: S51866
A:Molecule type: DNA
A:Residues: 1-752 <COLI>
A:Cross-References: EMBL:248179; NID:g665657; PIDN:CAA88220.1; PID:g665671; MIPS:YDR1
R:Aguilera, A.; Klein, H.L.
Mol. Cell. Biol. 10, 1439-1451, 1990
A>Title: HPRI, a novel yeast gene that prevents intrachromosomal excision recombinati
A:Reference number: A34781; MUID:90205821
A:Accession: A34781
A:Molecule type: DNA
A:Residues: 1-403, 'L', 405-752 <AGU>
A:Cross-References: EMBL:M30484; NID:g171701; PIDN:AAA34685.1; PID:g171702
C:Genetics:
A:Gene: SGD:HPRI
A:Cross-References: SGD:S0002545; MIPS:YDR138w
A:Map position: 4R
C:Superfamily: Saccharomyces cerevisiae HPRI protein

```


Db 37 KRLVNAEYLSWEPAVLSNST-----RPVYRVQPKYTDSKFTADINSIGVNCQTITA 91
OY 65 SFCDLDEMRSTHEAVTVLEGF--SGNTLL-----FSCSHNFWLAI-----DMSFEP 110
Db 92 TECDFTNAPSBA-----GFPMDPNTTLRLRAELGALHSMVMPQIHRNTVGP 142
OY 111 PEEFIVGFTNHINWVKFPS--IYEEELQFDLSLVIEQSEGIYKHKRPEIKGNSGNF 167
Db 143 PE-NIEVTVQEGSLIIRFSSPFDIADTSTAFCYVYHVMKGGI-----QVKGPFPSRN- 195
OY 168 TYIIDKLIPTNTYCVSV 184
Db 196 SISLDNLKPSRYCYLOV 212

RESULT 14

G01418
cytokine receptor family II, member 4 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C:Accession: G01418
R:Luftalla, G.
submitted to the EMBL Data Library, April 1994
A:Reference number: G06935
A:Accession: G01418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-273 <LUT>
A:Cross-references: EMBL:U08988; NID:g571295; PID:g571296
C:Genetics:
A:Gene: GDB:CRFB4; CRF2-4
A:Cross-references: GDB:138168; OMIM:123889
A:Map position: 21q22.1-21q22.2
A:Introns: 17/1; 58/2; 111/1; 166/3; 216/1

Query Match 7.8%; Score 89.5; DB 2; Length 273;
Best Local Similarity 22.8%; Pred. No. 1.5;
Matches 41; Conservative 28; Mismatches 74; Indels 37; Gaps 8;

OY 21 NFRSILSWE---LKNHSYFTHITLYTMSKPEDLKVKNCANTTRSCDLTDEMRSTH 77
Db 33 NFKNIIQWESPAPAKGNLTFTAQYLSYRIFQ-----DKCNTLLTECDF-----SSL 79
OY 78 EAVTVLEGFSGNTTL-----FSCSHNFWLAI-----DMSFEPPEPEIYGFTHINWV 126
Db 80 SKY-----GDHTLRVRAFEADEHSDWVNTIFCPYDITIGPPGQYEVLDSDLMRF 131
OY 127 KPFSIVEELQFDLSLVIEQSEGI-VKHKRPEIKGNSGNFTY-IIDKLIPTNTYCVSV 184
Db 132 LAPKIENEYETMTKMNVMYNSWTVNQVWKNGTDEKFOITPQYDFEVLRLNLEPWTYCYOV 191

RESULT 15

S67283

hypothetical protein YOR371c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein O6679

C:Species: Saccharomyces cerevisiae

C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000

C:Accession: S67283

R:Delius, H.; Hebling, U.; Hofmann, B.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67261

A:Accession: S67283

A:Molecule type: DNA

A:Residues: 1-897

A:Cross-references: EMBL:275279; NID:g1420801; PID:g1420802; GSPDB:GN00015; MIPS:YOR371c

A:Experimental source: strain S288C

C:Genetics:

A:Gene: MIPS:YOR371c

A:Map position: 15R

Query Match 7.8%; Score 89.5; DB 2; Length 897;
Best Local Similarity 21.2%; Pred. No. 7.4;
Matches 58; Conservative 28; Mismatches 68; Indels 119; Gaps 14;

OY 3 YDSPDYTDSCITK-----ISLRNFRSLSM-----ELKNHSI 35
Db 155 YDFEDNTDDECNKACHAFHYSSERLEILNRSTISFYKRLTLVDLRDSDVLRHNL 214
OY 36 ---VPTHTLLTYTMSKPE-----DLKVKNCANTTRSCDLTDEMRSTH 77
Db 215 WMPMTRRRFRFLVSSSKPEDVALTPIPRFSSDLDIRN--KTCPLTINGTD---CVP 269
OY 78 EAVTVLEGFSGNTTLFSCSHNFWLAI DMSFEPPEPEIYGFTHINWVKFPSIVEEIQ 137
Db 270 RSYDT---FSGSSVIASIF-----SEYKLPISLYHCSV-----ELN 302
OY 138 FDLSLVIEQSEGIYKHKR-----PEIKGNSGNFTYIIDK 173
Db 303 DQLEIV---GGLMACHRVDEAPDLKDYVDGIRNLPPPLIPELINPS----- 348
OY 174 LIPNTN-YCVSV---YLEHSDQAVIKSPKCT 202
Db 349 MIPPHLYCFSLTSSRLTRPDISGYIPPLVCT 381

Search completed: December 14, 2000, 10:28:22
Job time: 95 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2000, 10:30:40 ; Search time 16.07 Seconds
(without alignments)
429.418 Million cell updates/sec

Title: US-09-166-298-26_COPY_1_216
Perfect score: 1144
Sequence: 1 ISYSDPDYDESCFTFKISLR.....SPLKTLPLPGQESSESASFA 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues
Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1144	100.0	515 1	INR2_HUMAN
2	690.5	60.4	530 1	INR2_BOVIN
3	671.5	58.7	536 1	INR2_SHEEP
4	129	11.3	292 1	TE_BOVIN
5	110.5	9.7	295 1	TE_HUMAN
6	107.5	9.4	292 1	TE_RABBIT
7	107.5	9.4	295 1	TE_RAT
8	99	8.7	1501 1	CDR1_CANAL
9	98	8.6	1499 1	CDR2_CANAL
10	97	8.5	294 1	TE_MOUSE
11	95	8.3	752 1	HPRI_YEAST
12	94	8.2	557 1	INR4_HUMAN
13	90.5	7.9	325 1	CRF4_HUMAN
14	90.5	7.9	337 1	INGS_HUMAN
15	88	7.7	1238 1	PTPJ_MOUSE
16	86.5	7.6	997 1	T257_ECOLI
17	86	7.5	1888 1	CALE_CHICK
18	85	7.4	560 1	INR1_BOVIN
19	84.5	7.4	845 1	AMPN_LACTIC
20	84	7.3	988 1	DPOL_FOPPV
21	82	7.2	298 1	MYOD_CHICK
22	82	7.2	489 1	INGR_HUMAN
23	81.5	7.1	345 1	URIC_DROPS
24	81.5	7.1	560 1	INR1_SHEEP
25	81.5	7.1	1086 1	SYL_RICER
26	81	7.1	493 1	CAMA_CHICK
27	81	7.1	662 1	INR1_MOUSE
28	81	7.1	692 1	YLN9_CAEEL
29	79.5	6.9	479 1	PAP1_VARY
30	79.5	6.9	1301 1	SAC3_YEAST
31	79	6.9	894 1	DSCI_HUMAN
32	78.5	6.9	1912 1	PTPD_HUMAN
33	78	6.8	660 1	SCAG_XENLA

34	77.5	6.8	547 1	IF37_MOUSE	070194 mus musculus
35	77	6.7	428 1	YOP1_CAEEL	009302 caenorhabdi
36	77	6.7	2366 1	TOXB_CLODI	P18177 clostridium
37	76.5	6.7	335 1	G49B_MOUSE	064281 mus musculus
38	76.5	6.7	399 1	RPSD_THENA	P77994 thermotoga
39	76.5	6.7	423 1	MTB1_BACAM	P23941 bacillus am
40	76.5	6.7	798 1	V120_HSVG	P30003 herpes simp
41	75.5	6.6	277 1	Y833_METHA	058243 methanococ
42	75.5	6.6	474 1	TRPE_METHA	058475 methanococ
43	75.5	6.6	479 1	PAP1_VACCC	P21079 vaccinia vi
44	75.5	6.6	683 1	BGH3_PIG	011780 sus scrofa
45	75.5	6.6	1043 1	SYL_CHLPPN	Q92972 chlamydia p

ALIGNMENTS

RESULT	ID	INR2_HUMAN	STANDARD:	PRT:	515 AA.
AC	P48551:				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	INTERFERON-ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA-REC)				
DE	(TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR-2)				
CN	IFNAR2 OR IFNARB.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE: 96067138.				
RA	Luftalla G., Holland S.J., Cinato E., Monneron D., Reboul J.,				
RA	Rogers N.C., Smith J.M., Stark G.R., Gardiner K., Mogenssen K.E.,				
RA	Kerr I.M., Uze G.;				
RT	"Mutant USA cells are complemented by an interferon-alpha beta				
RT	receptor subunit generated by alternative processing of a new member				
RT	of a cytokine receptor gene cluster.";				
RL	EMBO J. 14:5100-5108(1995).				
RL	[2]				
RN	SEQUENCE FROM N.A. (SHORT FORM), AND PARTIAL SEQUENCE.				
RP	TISSUE=MONOCYTES;				
RA	MEDLINE: 94236684.				
RA	Novick D., Cohen B., Rubinstein M.;				
RT	"The human interferon alpha/beta receptor: characterization and				
RT	molecular cloning.";				
RL	Cell 77:391-400(1994).				
RL	[3]				
RN	SEQUENCE FROM N.A. (LONG FORM), AND FUNCTION.				
RP	MEDLINE: 95394915.				
RA	Domanski P., Witte M., Kellum M., Rubinstein M., Hackett R.,				
RA	Diana P., Colamonic O.R.;				
RT	"Cloning and expression of a long form of the beta subunit of the				
RT	interferon alpha beta receptor that is required for signaling.";				
RL	J. Biol. Chem. 270:21606-21611(1995).				
RL	[4]				
RP	SEQUENCE FROM N.A. (LONG FORM).				
RC	TISSUE=BLOOD;				
RA	Cohen B., Kim S.H., Novick D., Rubinstein M.;				
RL	Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.				
RL	[5]				
RP	DISCUSSION OF VARIOUS FORMS, AND PARTIAL SEQUENCE.				
RX	MEDLINE: 95279874.				
RA	Novick D., Cohen B., Tal N., Rubinstein M.;				
RT	"Soluble and membrane-anchored forms of the human IFN-alpha/beta				
RT	receptor.";				
RL	J. Leukoc. Biol. 57:712-718(1995).				
CC	-1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. THE LONG AND				
CC	SOLUBLE FORMS ARE DIRECTLY INVOLVED IN SIGNAL TRANSDUCTION DUE TO				
CC	THEIR INTERACTION WITH THE TYR KINASE, JAK1. THE LONG FORM ALSO				
CC	INTERACTS WITH THE TRANSCRIPTIONAL FACTORS, STAT1 AND STAT2. BOTH				

```
CC FORMS ARE POTENT INHIBITORS OF TYPE I IFN ACTIVITY.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A LONG FORM/IFNAR2-2 (SHOWN
CC HERE), A SHORT FORM/IFNAR2-1 AND A SOLUBLE FORM/IFNAR2-3/P40; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- P-TM: UPON BINDING, IFNAR2 IS PHOSPHORYLATED ON TYROSINE RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: LA2243: AAB46417.1: -.
DR EMBL: LA2238: AAB46417.1: JOINED.
DR EMBL: LA2239: AAB46417.1: JOINED.
DR EMBL: LA2240: AAB46417.1: JOINED.
DR EMBL: LA2241: AAB46417.1: JOINED.
DR EMBL: LA2242: AAB46417.1: JOINED.
DR EMBL: LA2243: AAB46418.1: -.
DR EMBL: LA2238: AAB46418.1: JOINED.
DR EMBL: LA2239: AAB46418.1: JOINED.
DR EMBL: LA2240: AAB46418.1: JOINED.
DR EMBL: LA2241: AAB46418.1: JOINED.
DR EMBL: LA2242: AAB46418.1: JOINED.
DR EMBL: LA2243: AAB46419.1: -.
DR EMBL: LA2238: AAB46419.1: JOINED.
DR EMBL: LA2239: AAB46419.1: JOINED.
DR EMBL: LA2240: AAB46419.1: JOINED.
DR EMBL: LA2241: AAB46419.1: JOINED.
DR EMBL: LA2242: AAB46419.1: JOINED.
DR EMBL: LA2243: AAB46419.1: JOINED.
DR EMBL: LA1944: AAB46415.1: -.
DR EMBL: LA1943: AAB46415.1: -.
DR EMBL: LA1944: AAB46413.1: -.
DR EMBL: LA1943: AAB46413.1: -.
DR EMBL: X77722: CAAS4785.1: -.
DR EMBL: U29584: AAC50202.1: -.
DR EMBL: X89772: CAA61914.1: -.
DR MIM: 602376: -.
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
KW Phosphorylation.
FT SIGNAL 1 26
FT CHAIN 27 515
FT DOMAIN 27 243 INTERFERON-ALPHA/BETA RECEPTOR BETA
FT TRANSMEM 244 264 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 245 515 POTENTIAL.
FT DISULFID 85 93 CYTOPLASMIC (POTENTIAL).
FT DISULFID 207 227 BY SIMILARITY.
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 240 331 SA -> FS (IN ISOFORM 2-3).
FT VARSPLIC 281 331 MISSING (IN ISOFORM 2-3).
FT VARSPLIC 331 331 NFNFTLAWFPNPPLPELADMDVYITINKKKKYNDYDE
FT SDSLTAAPR -> RQGLAKGNVAVAIHRCSHNAALQSETP
FT LKQSSCLSPSSWDYKRASLCPSD (IN ISOFORM 2-
FT 1).
FT VARSPLIC 332 515 MISSING (IN ISOFORM 2-1).
FT CONFLICT 10 10 F -> V (IN REF. 2 AND 4).
FT CONFLICT 151 151 M -> V (IN REF. 3).
SQ SEQUENCE 515 AA: 57758 MW: 4D7730D93AA739F4 CRC64;
```

```
QY 1 ISYDSPDYTESCTFKISLNRNRSILSMELKNHSIVPTHYLLTYLTKSKPEDLKVNCA 60
DB 27 ISYDSPDYTESCTFKISLNRNRSILSMELKNHSIVPTHYLLTYLTKSKPEDLKVNCA 86
QY 61 NTRRSFCDLIDEMRSTHEAVTVYLEGFSGNTTLFSCSHNWLAIADMSFEPPEFIYGF 120
DB 87 NTRRSFCDLIDEMRSTHEAVTVYLEGFSGNTTLFSCSHNWLAIADMSFEPPEFIYGF 146
QY 121 HINMVAKPSIVEEELQEDLSLVEESEGIVKHKPEIKGNMNGNTYIIDKLIPNTNY 180
DB 147 HINMVAKPSIVEEELQEDLSLVEESEGIVKHKPEIKGNMNGNTYIIDKLIPNTNY 206
QY 181 CVSYLLEHSDQAVIKSPILCTLLPQGESESASA 216
DB 207 CVSYLLEHSDQAVIKSPILCTLLPQGESESASA 242
RESULT 2
INR2_BOVIN STANDARD; PRT; 530 AA.
ID INR2_BOVIN
AC 095141;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA-REC)
DE (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR-
DE 2).
GN IFNAR2 OR IFNARB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM.
RX MEDLINE: 98006426.
RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
RT "Molecular cloning of ovine and bovine type I interferon receptor
RT subunits from uteri, and endometrial expression of messenger
RT ribonucleic acid for ovine receptors during the estrous cycle and
RT pregnancy."
RL Endocrinology 138:4757-4767(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. PROBABLY
CC INVOLVED IN SIGNAL TRANSDUCTION BY INTERACTING WITH THE TYR
CC KINASE, JAK1.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL: U75304: AAB4233.1: -.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 26
FT CHAIN 27 530
FT DOMAIN 27 246 INTERFERON-ALPHA/BETA RECEPTOR BETA
FT TRANSMEM 247 267 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 268 530 POTENTIAL.
FT DOMAIN 358 367 CYTOPLASMIC (POTENTIAL).
FT REPEAT 358 367 2 X 5 AA TANDEM REPEATS OF S-L-E-D-C.
FT REPEAT 363 367 1.
FT DISULFID 85 93 BY SIMILARITY.
FT DISULFID 210 230 BY SIMILARITY.
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
```

FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 530 AA; 59584 MM; 66A2C6D896B4DAD6 CRC64;
 Query Match 60.4%; Score 690.5; DB 1; Length 530;
 Best Local Similarity 60.3%; Pred. No. 1,1e-53;
 Matches 133; Conservative 30; Mismatches 52; Indels 5; Gaps 2;
 QY 1 ISYSPDYTDSCFKISLRNFRSILSMELKNHSIVPHYLLTITMSKPEDLKVKNCA 60
 DB 27 ISYAPPLSDCHCLKMFNFQSVLSMELKNHSIVPHYLLTITMSKREDMAYVADCI 86
 QY 61 NITRSFCDLTDWMSRTHAAYTVLEGFSGNTLFCSCSHNFWLADMSPEPEFIVGFTN 120
 DB 87 NITRSFCDLTDWVNTDMYIPQVGFRENKLVTCMGSEFLVPDPLDPPEFIVGFTN 146
 QY 121 HINWVRF---PSIVEELOFDLSVIEOSEGIVKKHKEIGNMSGNTYIIDKLIP 176
 DB 147 HISVNVKRFQSDSPGILSEELQFYLAFL-IEEHAGNSVKRHQPOITGNITKNENYVIDKLIP 205
 QY 177 NTNVCVSYLHSDQAVIKSPKCTLLPQGESESAESA 216
 DB 206 NTNVCISYFEPKDPKRNKINSPLKCTLFRPRESESESA 245
 RESULT 3
 INR2_SHEEP STANDARD; PRT; 536 AA.
 AC Q95207;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA-REC-2).
 GN IFNAR2 OR IFNAR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ENDOMETRIUM;
 RX MEDLINE: 98006426.
 RA Han C.-S., Mathalagan N., Klemann S.W., Roberts R.M.: "Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and pregnancy."
 RT Endocrinology 138:4757-4767(1997).
 RL Endocrinology 138:4757-4767(1997).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. PROBABLY INVOLVED IN SIGNAL TRANSDUCTION BY INTERACTING WITH THE TYR KINASE, JAK1.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT CONCEPTUS AT DAY 15 OF PREGNANCY.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC -----
 DR EMBL: U65979; AAB84232.1; -.
 DR INTERPRO: IPR001777; -.
 DR PFM: PF00041; fn3; 1.
 KM Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 536
 FT CHAIN CHAIN.

FT DOMAIN 27 246
 FT TRANSMEM 247 267
 FT DOMAIN 268 536
 FT DOMAIN 358 372
 FT REPEAT 358 362
 FT REPEAT 363 367
 FT REPEAT 368 372
 FT DISULFID 85 93
 FT DISULFID 210 230
 FT CARBOHYD 58 58
 FT CARBOHYD 87 87
 FT CARBOHYD 101 101
 FT CARBOHYD 147 147
 FT CARBOHYD 191 191
 SQ SEQUENCE 536 AA; 60260 MM; 1055F27D80545150 CRC64;
 Query Match 58.7%; Score 671.5; DB 1; Length 536;
 Best Local Similarity 59.1%; Pred. No. 5,3e-52;
 Matches 130; Conservative 32; Mismatches 53; Indels 5; Gaps 2;
 QY 1 ISYSPDYTDSCFKISLRNFRSILSMELKNHSIVPHYLLTITMSKPEDLKVKNCA 60
 DB 27 ISYAPPLSDCHCLKMFNFQSVLSMELKNHSIVPHYLLTITMSKPEDMAYVADCI 86
 QY 61 NITRSFCDLTDWMSRTHAAYTVLEGFSGNTLFCSCSHNFWLADMSPEPEFIVGFTN 120
 DB 87 NITRSFCDLTDWVNTDMYIPQVGFRENKLVTCMGSEFLVPDPLDPPEFIVGFTN 146
 QY 121 HINWVRF---PSIVEELOFDLSVIEOSEGIVKKHKEIGNMSGNTYIIDKLIP 176
 DB 147 HISVNVKRFQSDSPGILSEELQFYLAFL-IEEHAGNSVKRHQPOITGNITKNENYVIDKLIP 205
 QY 177 NTNVCVSYLHSDQAVIKSPKCTLLPQGESESAESA 216
 DB 206 NTNVCISYFEPKDPKRNKINSPLKCTLFRPRESESESA 245
 RESULT 4
 TF_BOVIN STANDARD; PRT; 292 AA.
 ID TF_BOVIN
 AC P30931;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).
 GN F3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-ADRENAL GLAND;
 RX MEDLINE: 92109720.
 RA Takayanoki Y., Muta T., Miyata T., Iwanaga S.: "cDNA and amino acid sequences of bovine tissue factor."
 RL Biochem. Biophys. Res. Commun. 181:1145-1150(1991).
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES FACTORS IX OR X BY SPECIFIC LIMITED PROTOCOLS. TF PLAYS A ROLE IN NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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CC or send an email to license@isb-sib.ch).

DR	EMBL:	J02931:	AAAG1150.1:	-
DR	EMBL:	M16553:	AAAG1151.1:	-
DR	EMBL:	J02846:	AAAG1152.1:	-
DR	EMBL:	M27436:	AAAG1154.1:	-
DR	EMBL:	A19048:	CAA01438.1:	-
DR	PIR:	A28320:	KEH03.	
DR	PIR:	A43645:	A43645.	
DR	PIR:	A47574:	A47574.	
DR	PDB:	1BOY:	10-JUN-96.	
DR	PDB:	2HFT:	29-JAN-96.	
DR	PDB:	1DAN:	04-SEP-97.	
DR	PDB:	1TFH:	25-FEB-98.	
DR	PDB:	1AHW:	19-AUG-98.	
DR	PDB:	1TFH:	19-AUG-98.	
DR	PDB:	1EAK:	03-DEC-99.	
DR	MM:	134390:	-	
DR	INTERPRO:	IPR001187:	-	
DR	PFAM:	PF01108:	Tissue_fac. 1.	
DR	PRINTS:	PRO0346:	TISSUEFACTOR.	
DR	PROSITE:	PS00621:	TISSUE_FACTOR; 1.	
KW	Glycoprotein:	Blood coagulation;	Transmembrane; Signal; Lipoprotein.	
KW	Palmitate:	3D-structure.		
FT	SIGNAL	1	32	
FT	CHAIN	33	295	
FT	DOMAIN	33	251	TISSUE_FACTOR.
FT	TRANSMEM	252	274	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	275	295	POTENTIAL.
FT	SITE	46	48	CYTOLASMIC (POTENTIAL).
FT	SITE	77	79	WKS MOTIF.
FT	SITE	190	192	WKS MOTIF.
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	169	169	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	81	89	
FT	DISULFID	218	241	
FT	LIPID	277	277	PALMITATE.
FT	CONFLICT	260	260	V-> A (IN REF. 4).
Q	SEQUENCE	295 AA:	33067 MW:	D3486C713EBEAD0 CRC64;

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Query Match Similarity      9.4% Score 107.5; DB 1; Length 292;
Best Local Similarity      25.2%; Pred. No. 0.018;
Matches    58; Conservative   37; Mismatches    68; Indels     67; Gaps    13;

Oy       21 NERSILSMELKNHSIVPTHYLLTYLIMSKEPDLYKVVNCANTNSFCDLTDE---WRST 76
          ||::||| | | | : - - - - - || :: : | : | : | | | | |
Db        48 NEKTILEMEPKSIDV---YTV--DISTRLENWK--SKCFLEATEECULTEBVVKDVGT 100
          + + + + + | + + + + + | + + + + + | + + + + + | + + + + +
Oy       77 HEAVYTVEGSGNNTFCSCSHNFALIDMSREPEPELVCGTNNINMMVPSPIVE-EE 135
          + + + + + | + + + + + | + + + + + | + + + + + | + + + + +
Db       101 YMARVLSPARGNGTGTF-----PEEPFRNSPETPLDNLNGLOPTIQSEQ 148
          + + + + + | + + + + + | + + + + + | + + + + + | + + + + +
Oy       136 LQFDLSLVIEEGSEGIGKKHKPEI-----KGNSGNFT-----YYI 171
          + + + + + | + + + + + | + + + + + | + + + + + | + + + + +
Db       149 VGTKINTWYVD-APTLVRRNGCTSLRAVFGRDLNYTLYWRASTGGTKATATTNEFLI 207
          + + + + + | + + + + + | + + + + + | + + + + + | + + + + +
Oy       172 DKLINTNVCVSYVLEHSDQAVT-----KSP---LKCTLTPPGQISE 211
          + + + + + | + + + + + | + + + + + | + + + + + | + + + + +
Db       208 D-VDRGENVCFSV-----QAVIDSRKRKORSSPESLTETCSREGGRARE 249
          + + + + + | + + + + + | + + + + + | + + + + + | + + + + +

RESULT           7
TF_RAT ID TF RAT STANDARD PRT: 295 AA.

AC P42533:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DN TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).
CN CFS.
OS Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Rosenfield C., Guha A., Nemerson Y., Taubman M.B.;
RL Submitted (Mar-1994) to the EMBL/Genebank/DBJ databases.
CC -I- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTOPLYSIS. TF PLAYS A ROLE IN
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -----
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CC -----
CC EMBL: U07619; AAA16966.1; -.
DR HSSP; P13726; 1TPH.
DR INTERPRO; IPRO01187; -.
DR PFAM; PF01108; Tissue_fac; 1.
DR PRINTS; PR00346; TISSUEFACTOR.
DR PROSITE; PS00621; TISSUE_FACTOR; 1.
KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW Palmitate.
FT SIGNAL 1 28
FT CHAIN 29 295 BY SIMILARITY.
FT DOMAIN 29 252 TISSUE FACTOR.
FT TRANSMEM 253 275 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 276 295 POTENTIAL.
FT SITE 246 248 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 38 38 WKS MOTIF.
FT CARBOHYD 58 58 N-LINKED (GLCNAc . . . ) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAc . . . ) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAc . . . ) (POTENTIAL).
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FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 76 84 BY SIMILARITY.
FT DISULFID 219 242 BY SIMILARITY.
FT LIPID 276 276 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 295 AA; 33443 MW; E84C15B4E3628D48 CRC64;

Query Match 9.4%; Score 107.5; DB 1; Length 295;
Best Local Similarity 26.8%; Pred. No. 0.018;
Matches 60; Conservative 23; Mismatches 74; Indels 67; Gaps 13;

OY 21 NFRSLTSEMLKHSIVPHYTLTYIMSPEDLKVVKNCAMTFSFCUTDE-----MR 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 45 DPKTLLEMQPK-----PKNYT--TYVQISDSRNNKKYCTGTTDECDLTDEIVADVW- 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 75 STHEAVYTVL---EGSGNTTLFSCSHNFWLAIIDMSPEPEEIVGFNNHIVVKKPSI 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 97 -TYEARVLISVPMRNSHTGKETLFG-TH-----GEEPPFTNARKFLPYRDTKIGQVVI 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 132 VEEELQFDLSLVEIQSEGIYKKHNP-----EIKNNMG-----NFTYII 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 147 QVEEGGTRKLKVTYKDSFTLVKKNCFLLTLRVFPENDLGYLTVRKDSSTGRKNTWTHTN 206
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 172 DKLI--PNTNVSQVSYLEHSDQAVI-----KSP---LKCT 202
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 207 EFLIDVEKGVSTCFPA-----QAVFSRKTNHKSPESTIKCT 243

RESULT 8
CDRL_CANAL
ID CDRL_CANAL STANDARD: PRT; 1501 AA.
AC P43071.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MULTIDRG RESISTANCE PROTEIN CDRL.
GN CDRL.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC anamorphic Saccharomycetales; Candida.
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN-ATCC 64385 / 1001;
RA MEDLINE: 95339406.
RX Pressed R., de Wergifosse P., Balzi E., Goffeau A.;
RT "Molecular cloning and characterization of a novel gene of Candida
RT albicans, CDRL, conferring multiple resistance to drugs and
RT antifungals.";
RL Curr. genet. 27:320-329(1995)
CC -I- FUNCTION: TRANSPORTER, WHOSE PHYSIOLOGICAL FUNCTION IS NOT YET
CC ESTABLISHED. CONFERS RESISTANCE TO THE CHEMICAL CYCLOHEXIMIDE.
CC -I- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS). PDRS SUBFAMILY.
CC -----
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CC -----
CC EMBL, X77589; CAA54692.1; -.
CC INTERPRO: IPR001617; -.
CC PFM: PFM0005; ABC_tran. 2.
CC PROSITE: PS00211; ABC_TRANSPORTER. 1.
CC ATP-binding; Transmembrane; Glycoprotein; Transport; Repeat.
KM DOMAIN 1 513 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 514 534 POTENTIAL.
FT TRANSMEM 549 569 POTENTIAL.
FT TRANSMEM 598 618 POTENTIAL.
FT TRANSMEM 623 643 POTENTIAL.

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Query Match	Best Local Similarity	8.2%	Score 94:	DB 1:	Length 557:
Matches 50;	Conservative 27;	Mismatches 88;	Indels 54;	Gaps 11;	

OY	21	NFRSLTSEIKHSH;VPPIHYLLTYLIMSKPBDKLVKKNACTNTSFCOLDENSTHEAY	80
		: :	:
Dd	44	NN--ILRMNRSDSEGANTFSPFOJKTGMWNK-LSCQNTPTSKCFSSKLKNVEEI	100
OY	81	VYLEGEGGNITLFSGSHNFWLAIDMSE-----PPFEIVGTTHINWVKFPSTV	132
	:		: :
Dd	101	KRIAAEKENT-----SSWEVD-STTPPKAIGPPEVHLEMDAKIYIHIS-PETK	151
OY	133	E-----ELOFDLSLVI-----EOSSEGIIVKKHKPEIKGNMSGNFYIIDKLIPNTN	179
	:	: : : :	: :
Dd	152	DSVMALDGLSFETYSLTIWMKNSGVEEERIENIYSRHK-----IYKLSPETT	197
OY	160	YCVSYVLEHSDQAV-IKSPDK-----TLTPQEASE	211
	:	: : :	: :
Dd	198	YCLKVAALLTSWKIGVSPVHCIKTVENELPENIE	236
<hr/>			
RESULT_13			
CREF4_HUMAN	ID	STANDARD:	PRT: 325 AA.
AC	008334;		
DT	01-FEB-1995	(Rel. 31, Created)	
DI	01-FEB-1995	(Rel. 31, Last sequence update)	
DI	01-OCT-1996	(Rel. 34, Last annotation update)	
DE	CYTOKINE RECEPTOR CLASS-II CR2-4 PRECURSOR.		
CN	CRFB4.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=FETAL BRAIN;		
RX	MEDLINE: 93300510.		
RA	Lutifalla G., Gardiner K., Uze G.;		
RT	"A new member of the cytokine receptor gene family maps on chromosome		
RT	21 at less than 35 kb from IFNAR."		
RL	Genomics 16:366-373(1993).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE: 96054036.		
RA	Lutifalla G., McInnis M.G., Antonarakis S.E., Uze G.;		
RT	"Structure of the human CRFB4 gene: comparison with its IFNAR		
RT	neighbor";		
RL	J. Mol. Evol. 41:338-344(1995).		
CC	- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.		
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	- SIMILARITY: CONTAINS 2 FIBROECTIN TYPE III-LIKE DOMAINS.		
CC	- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL: Z17227; CAAT8933.1; -;		
DR	EMBL: 008988; AAA86872.1; -;		
DR	PIR: A47003; A47003.		
DR	HSSP: P13726; IDAN.		
DR	MIM: 123889; -;		
KW	Receptor; Transmembrane; Glycoprotein; Signal.		
FT	SIGNAL	1	19
FT	CHAIN	20	325
FT	DOMAIN	20	220
FT	TRANSMEM	221	249
FT	DOMAIN	250	325
FT	DISULFD	188	209
FT	DISULFD	49	49
FT	CARBOHYD	68	68
FT	CARBOHYD	68	68
<hr/>			
N-LINKED (GLCNAC. . .) (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL).			

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FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 124 124 A -> D (IN REF. 2).
FT CONFLICT 269 273 FLGHP -> VGRME (IN REF. 2).
FT CONFLICT 274 325 MISSING (IN REF. 2).
SQ SEQUENCE 325 AA: 37011 MM: 66706C79F8514B23 CRC64;

Query Match
Best Local Similarity 7.9%; Score 90.5; DB 1; Length 325;
Matches 41; Conservative 28; Mismatches 74; Indels 37; Gaps 8;

QY 21 NFNISLSWE---LKNHSIVPTHLLTYTMSKPEDLKVNKNCANTTSFCDLDEMSTH 77
DB 33 NFNILQWESPAPAKGNLFTAOYLSYRFO-----DKCMWTLTECDF-----SSL 79

QY 78 EAVVTYVLEGSNTLT-----FSCSHNFWLAI-----DMSFPEPEFEIYGFTHNWV 126
DB 80 SKT-----GDHTLVRAEFDHSDWNTFCPVDDTTIGPGMQVEVLADSLMRF 131

QY 127 KFPSIVEEELQFDLSLYIEOSEGI-VKHKHPEIKGMSGNFY-IIDKLIPNTNYCSV 184
DB 132 LAKRIENEYETWTKMKNYNSMTYVVOYWKNGTDEKFIITPOYDEVLARNLEPWTTTCVQV 191

RESULT 14
INCS_HUMAN STANDARD; PRT; 337 AA.
AC P384B4;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
GN IFNGR2 OR IFNGT1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP TISSUE=LUNG.FIBROBLAST;
RX MEDLINE: 94170380.
RA Soh J., Donnelly R.J., Kotenko S., Maritano T.M., Cook J.R.,
Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;
RT "Identification and sequence of an accessory factor required for
activation of the human interferon gamma receptor.";
RL Cell 76:793-802(1994).
RN [2]
RP SEQUENCE OF 1-24 FROM N.A.
RX MEDLINE: 97067142.
RA Rhee S., Ebersperger C., Dembic Z., Pestka S.;
RT "The structure of the gene for the second chain of the human
interferon gamma receptor.";
RL J. Biol. Chem. 271:28947-28952(1996).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR
SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF
THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO
INTERACT WITH GAF, JAK1, AND/OR JAK2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U05875; AAA16955.1; -
DR EMBL: U05877; AAA16956.1; -
DR EMBL: U06755; AAC52066.1; -

```

```

DR MTM; 147569; -.
DR INTERPRO: IPR001777; -.
DR PFAM: PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 27
FT CHAIN 28 337
FT DOMAIN 28 247
FT TRANSMEM 248 268
FT DOMAIN 269 337
FT CARBOHYD 85 85
FT CARBOHYD 110 110
FT CARBOHYD 137 137
FT CARBOHYD 219 219
FT CARBOHYD 231 231
FT VARIANT 64 64
SQ SEQUENCE 337 AA: 37834 MM: 18C61B10AD90E309 CRC64;
/FTID=VAR_002718.

Query Match
Best Local Similarity 7.9%; Score 90.5; DB 1; Length 337;
Matches 48; Conservative 26; Mismatches 74; Indels 49; Gaps 11;

QY 16 KISLNRFRSLSWE---LKNHSIVPTHLLTYTMSKPEDLK-----VKNKCANFTR 64
DB 37 KIRLYNAEOYLSWEPVALNST-----RPVYVRVQFYTSKMTADIMSIGVCTQITA 91

QY 65 SFCDLTDEMSTHAAVYVLEGF---SGNTLT-----FSCSHNFWLAI-----DMSFEP 110
DB 92 TECDFTAASPSA-----GFPMDNFVTLRLRAELGALHSAAVTPMPOHRYNVTGP 142

QY 111 PEFIVGFTHNINVMKFPS---IVEELOFDLSLYIEOSEGI-VKHKHPEIKGMSGNF 167
DB 143 PE-NIEVTPBGSLILIRFSSPEFDIADISTAFPCYVHWKNGCI-----QVAKPFRSN- 195

QY 168 TYIIDKLIPNTNYCSV 184
DB 196 SISLNLKPSRYVCLQV 212

RESULT 15
PRT_MOUSE STANDARD; PRT; 1238 AA.
ID PRT_MOUSE
AC 064455;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR (EC 3.1.3.48) (R-PTP-ETA)
DE (HPTP BETA-LIKE TYROSINE PHOSPHATASE).
GN PTPRJ OR BTP.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MRL-LPR/LPR;
RX MEDLINE: 96140699.
RA Kuranochi S., Matsuda S., Satoh T., Ohnogi M.,
Yamamoto T.;
RT "Molecular cloning and characterization of BTP, a murine
receptor-type tyrosine phosphatase similar to human DEP-1.";
RL FEBS Lett. 378:7-14(1996).
CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
PROTEIN TYROSINE + PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN EVERY TISSUE EXAMINED.
CC -1- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
CC -1- SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its

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...

FT /label= see above
 FT Modified-site 192..194
 FT /label= see above
 XX
 XX A09511416-A.
 PD 17-AUG-1995.
 PD
 XX 27-JAN-1995; 95AU-0011416.
 PF
 XX 07-FEB-1994; 94IL-0108584.
 PR
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (COHE/) COHEN B.
 XX
 PI Cohen B, Novick D, Rubinstein M;
 XX
 DR WPI; 1995-311811/41.
 DR N-PSDB; T04580.
 XX
 PT New DNA encoding interferon alpha/beta binding protein - useful for
 PT treating auto:immune diseases, inflammation and toxicity due to
 PT interferon treatment
 XX
 PS Disclosure; Fig 4; 82pp; English.

CC An oligo (T04579) corresp. to a non-degenerate internal sequence of
 CC IFNAB-BPI was synthesised, end-labeled and used for screening of cDNA
 CC libraries. Screening of a lambda gt11 cDNA library of human HeLa cells
 CC gave several positive clones. One of these clones is designated q10
 CC (T04576). Sense and antisense primers, corresp. to ends of the nt.
 CC sequence 219-613 of clone q10 were used for preparing a specific probe
 CC by PCR, using clone q10 as a DNA template. A human monocycle cDNA library,
 CC constructed in phage lambda pCEV9, was then screened with a 397 bp
 CC probe made by PCR from the coding region of clone q10. 22 clones
 CC were isolated with a 1.5 kb insert and two clones with a 4.5 kb
 CC insert. DNA sequence analysis of two 1.5 kb clones (T04580), as
 CC well as the entire ORF of two 4.5 kb clones (T04581) was performed.
 CC The 1.5kb clones coded for the same precursor of the transmembrane
 CC protein that was coded from by clone q10. The 1.5 kb clones codes
 CC for complete precursor of IFNAB-1, which is a cell surface
 CC receptor. The protein and CNBR peptide sequences (see R80068 and
 CC R80064), obtd. from urinary IFNAB-BP were all identified within
 CC the translated DNA sequence. Partial sequencing of the two 4.5 kb
 CC clones revealed the same 5' sequence of 237 codons as present in
 CC the 1.5 kb clones, followed by a different sequence. The 4.5 kb
 CC cDNA codes for a precursor of a truncated soluble receptor which
 CC is IFNAB-BPII, identical in its C-terminal sequence to the
 CC one isolated from urine. The two mRNAs coding for the precursor
 CC proteins of both IFNAB-BPI and IFNAB-BPII are derived from the
 CC same gene, probably by alternative splicing.
 XX
 XX Sequence 331 AA:

Query Match 100.0%; Score 1144; DB 16; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1.8e-106;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVDSPTVTESCFKISLRNFRSLSMELKNHSIVPTHTLTLYTMSKPEDLKVVNCA 60
 DB 27 ISYDSPYLTDESCTFKISLRNFRSLSMELKNHSIVPTHTLTLYTMSKPEDLKVVNCA 86
 QY 61 NTRRSPFDLDEMRSTHEAVTVLEGFSGNNTLFSCHNFMFLADMSFEPEPEFIVGFTN 120
 DB 87 ntrrsfcdldemrstheavtvlegrfsgntllfscshnfialdmsfepfefivgftn 146
 QY 121 HINVMKFSPIVEEELQFDLSLVTEQSEGLVKKHKPEIKCNMSGNFTYIIIDKLPIPTNY 180
 DB 147 hlnvmkfpsiveeelqfdlsilvaeqseqlvkhhkpeikgmsgnftlyiidklpiptny 206
 QY 181 CAVSYLEHSDQAVIKSPKLTLLPQOESASASA 216
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 207 cvsytlehsdegavikspkltllppqsesasa 242

RESULT 2

ID R80063 standard; Protein; 265 AA.

AC R80063;

DT 25-JAN-1996 (first entry)

XX Human IFNAB-BPI encoded in clone q10.

XX Interferon alpha/beta binding protein; IFNAB-BPI;
 KW cytokine binding protein; soluble cytokine receptor.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..26
 FT /label= signal peptide

FT Domain 244..264
 FT /label= transmembrane domain

FT Peptide 1..28
 FT /label= N-terminus peptide 1 (n1)

FT Peptide 29..47
 FT /label= n2

FT Peptide 72..91
 FT /label= CNBR peptide 3 (cb3)

FT Peptide 151..177
 FT /label= cb7

FT Peptide 189..207
 FT /label= cb6

XX A09511416-A.

XX 17-AUG-1995.

XX 27-JAN-1995; 95AU-0011416.

PF 07-FEB-1994; 94IL-0108584.

PR (YEDA) YEDA RES & DEV CO LTD.

PA (COHE/) COHEN B.

XX Cohen B, Novick D, Rubinstein M;

XX WPI; 1995-311811/41.

DR N-PSDB; T04576.

XX New DNA encoding interferon alpha/beta binding protein - useful for

PT treating auto:immune diseases, inflammation and toxicity due to

PT interferon treatment

XX Claim 19; Fig 2; 82pp; English.

XX A sample of urinary IFNAB-BP, obtd. as described in Israeli Patent

CC Application No 106591, was digested with CNBR. Seven discrete

CC peptide bands, designated cb1-cb7, were resolved. One of the

CC peptides, cb7, was smaller than 10,000 and gave the internal

CC sequence in R80064 (Met precedes the actual sequence). The internal

CC sequence was reverse-translated into sense (AAs 1-8) (T04577) and

CC antisense (AAs 27-20) (T04578) primers. Decanucleotides and

CC nonanucleotides, contg. the BamHI and SalI sites, respectively, were

CC added to the 5' ends of the primer oligos. Total RNA was purified

CC from human cells and first strand cDNA was generated with reverse

CC transcriptase, using either the antisense oligo mixture or

CC oligo d(T) as a primer. The PCR products included a 101 bp oligo

CC band which encoded the expected sequence from CNBR peptide cb7,

CC residues 9-20 (R80065). An oligo (T04579) corresp. to this

CC non-degenerate internal sequence was synthesised, end-labeled

CC and used for screening of cDNA libraries. Screening of a lambda

CC gt11 cDNA library of human HeLa cells gave several positive clones.


```
RESULT 4
ID Y25370 standard; peptide; 400 AA.
XX
AC Y25370;
XX
DT 06-SEP-1999 (first entry)
XX
DE IFNAR2/IFN-beta complex protein.
XX
KM IFNAR2; IFN-beta; type I interferon; IFNAR/IFN complex; IFN; antiviral;
human interferon alpha/beta receptor; antitumor; immunomodulatory;
anti-arthritic; antidiabetic; treatment; hepatitis; viral infection;
hairy cell leukemia; Kaposi's sarcoma; multiple myeloma; cancer; lupus;
diabetes; multiple sclerosis; rheumatoid arthritis; myasthenia gravis;
acquired immune deficiency syndrome.
XX
OS Synthetic.
XX
PN WO932141-A1.
XX
PD 01-JUL-1999.
XX
PF 18-DEC-1998; 98WO-US26926.
XX
PR 19-DEC-1997; 97US-0068295.
XX
PA (ISTP ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PA (MCIN/) MCINNIS P G.
XX
PI Cunningham M, El Tayar N, McKenna S, Sherris D;
PI Tepper M;
XX
DR WPI; 1999-405115/34.
XX
PT Prolonging in vivo activity of type I interferon by complexing
XX
PS Example 8; Page 80-82; 86pp; English.
XX
CC This invention describes a novel method for prolonging the in vivo effect
of type I interferon (IFN) by administering IFN as a complex (A) with a
subunit (I) of the human interferon alpha/beta receptor (IFNAR). The
product of the invention has antiviral, antitumor, immunomodulatory,
anti-arthritic and antidiabetic activity. (A) have the antiviral,
antitumor and immunomodulating activities of IFN, e.g. for treating
hepatitis and other viral infections, hairy cell leukemia, Kaposi's
sarcoma, multiple myeloma and other cancers, multiple sclerosis,
rheumatoid arthritis, myasthenia gravis, diabetes, acquired immune
deficiency syndrome and lupus. When complexed in (A), the storage life of
IFN is increased (i.e. it is stabilized against oligomerization, without
the need for storage at acidic pH) and its biological effect is
potentiated.
CC
CC
CC
CC
XX
SQ Sequence 400 AA;

Query Match 98.2%; Score 1123; DB 20; Length 400;
Best Local Similarity 100.0%; Pred. No. 3e-104;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 181 CVAHYLEHSDQAVIKSPKCTLLPGQESE 211
DB 207 CVAHYLEHSDQAVIKSPKCTLLPGQESE 237

RESULT 5
ID Y25371 standard; peptide; 415 AA.
XX
AC Y25371;
XX
DT 06-SEP-1999 (first entry)
XX
DE IFNAR2/IFN-beta complex protein.
XX
KM IFNAR2; IFN-beta; type I interferon; IFNAR/IFN complex; IFN; antiviral;
human interferon alpha/beta receptor; antitumor; immunomodulatory;
anti-arthritic; antidiabetic; treatment; hepatitis; viral infection;
hairy cell leukemia; Kaposi's sarcoma; multiple myeloma; cancer; lupus;
diabetes; multiple sclerosis; rheumatoid arthritis; myasthenia gravis;
acquired immune deficiency syndrome.
XX
OS Synthetic.
XX
PN WO932141-A1.
XX
PD 01-JUL-1999.
XX
PF 18-DEC-1998; 98WO-US26926.
XX
PR 19-DEC-1997; 97US-0068295.
XX
PA (ISTP ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PA (MCIN/) MCINNIS P G.
XX
PI Cunningham M, El Tayar N, McKenna S, Sherris D;
PI Tepper M;
XX
DR WPI; 1999-405115/34.
XX
PT Prolonging in vivo activity of type I interferon by complexing
XX
PS Example 8; Fig 10; 86pp; English.
XX
CC This invention describes a novel method for prolonging the in vivo effect
of type I interferon (IFN) by administering IFN as a complex (A) with a
subunit (I) of the human interferon alpha/beta receptor (IFNAR). The
product of the invention has antiviral, antitumor, immunomodulatory,
anti-arthritic and antidiabetic activity. (A) have the antiviral,
antitumor and immunomodulating activities of IFN, e.g. for treating
hepatitis and other viral infections, hairy cell leukemia, Kaposi's
sarcoma, multiple myeloma and other cancers, multiple sclerosis,
rheumatoid arthritis, myasthenia gravis, diabetes, acquired immune
deficiency syndrome and lupus. When complexed in (A), the storage life of
IFN is increased (i.e. it is stabilized against oligomerization, without
the need for storage at acidic pH) and its biological effect is
potentiated.
CC
CC
CC
CC
XX
SQ Sequence 415 AA;

Query Match 98.2%; Score 1123; DB 20; Length 415;
Best Local Similarity 100.0%; Pred. No. 3.1e-104;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	121	HNVMVKPFSSIVEELQFPLSLVIEEQSGIYKHKHPEIKGMNMGCFYTIIDKLI	PNTNY	180
Db	147	hnmvmkfpssiveelqfplslvieeqsgiykhhkpeikgmnmgnfytildkllpntny		206
QY	181	CVSYYLEHSDQAVIKSPKLTCLLPQGESE	211	
Db	207	cvsyylehsedegavikspikctllppqge	237	
RESULT	6			
R80064				
ID	R80064	standard; peptide: 27 AA.		
XX				
AC	R80064;			
XX				
DT	25-JAN-1996	(first entry)		
XX				
DE	Internal CNR peptide cb7 from IFNAB-BPI.			
XX				
KM	Interferon alpha/beta binding protein; IFNAB-BPI;			
KM	cytokine binding protein; soluble cytokine receptor.			
XX				
OS	Homo sapiens.			
XX				
PN	AU9511416-A.			
XX				
PD	17-AUG-1995.			
XX				
PF	27-JAN-1995; 95AU-0011416.			
XX				
PR	07-FEB-1994; 94IL-0108584.			
XX				
PA	(YEDA) YEDA RES & DEV CO LTD.			
PA	(COHE/) COHEN B.			
XX				
PI	Cohen B, Novick D, Rubinstein M;			
XX				
DR	WPI; 1995-311811/41.			
XX				
PT	New DNA encoding interferon alpha/beta binding protein - useful for			
PT	treating auto-immune diseases, inflammation and toxicity due to			
PT	interferon treatment			
XX				
PS	Disclosure; Fig 1A; 82pp; English.			
XX				
CC	A sample of urinary IFNAB-BP, obtd. as described in Israeli Patent			
CC	Application No 106591, was digested with CNBR. Seven discrete			
CC	peptide bands, designated cb1-cb7, were resolved. One of the			
CC	peptides, cb7, was smaller than 10,000 and gave the internal			
CC	sequence in R80064 (Met precedes the actual sequence). The internal			
CC	sequence was reverse-translated into sense (AAs 1-8) (T04577) and			
CC	antisense (AAs 27-20) (T04578) primers. Decanucleotides and			
CC	nonanucleotides, contg. the BamHI and SalI sites, respectively, were			
CC	added to the 5' ends of the primer oligos. Total RNA was purified			
CC	from human cells and first strand cDNA was generated with reverse			
CC	transcriptase, using either the antisense oligo mixture or			
CC	oligo d(T) as a primer. The PCR products included a 101 bp oligo			
CC	band which encoded the expected sequence from CNR peptide cb7.			
XX				
SO	Sequence 27 AA:			
	Query Match	11.3%; Score 129; DB 16; Length 27;		
	Best Local Similarity	100.0%; Pred. NO. 1.6e-06;		
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	125	MVKPFSIVEELQFPLSLVIEEQSGI	151	
Db	1	mvkfpssiveelqfplslvieeqsg	1	
RESULT	7			
	725405			

[illegible]

RESULT	8	
Y25406		
ID	Y25406	standard; Protein; 287 AA.
XX		
AC	Y25406;	
XX		
DT	08-SEP-1999	{first entry}
XX		
DE	Human tissue factor clone NuV124 protein.	
XX		
FW	Tissue factor; human; thrombogenic; substructure; thrombose; tumour;	
KW	vasculative malformation; vascular endothelium; NuV124.	
XX		
OS	Homo sapiens.	
XX		
PN	W09932143-A1.	
XX		
PD	01-JUL-1999.	
XX		
PF	22-DEC-1998;	98WO-US27498.
XX		
PR	23-DEC-1997;	97US-0996744.
XX		
PA	(NuVA-) NuVAS LLC.	
XX		
PI	Dickinson CD, Houston LL;	
XX		
DR	WPI; 1999-405116/34.	
DR	N-PSDB; X78883.	
XX		
PT	New thrombogenic polypeptides used to, e.g. obliterate vasculative	
XX	malformations	
CS	Claim 30; Page 78-81; 97pp; English.	

[illegible]

RESULT	9	
Y25407		
ID	Y25407	standard; protein; 351 AA.
XX		
AC	Y25407;	
XX		
DT	08-SEP-1999	(first entry)
XX		
DE	Human tissue factor clone NuV125 protein.	
XX		
KW	Tissue factor; human; thrombogenic; substructure; thrombose; tumour;	
KW	vasculative malformation; vascular endothelium; NuV125.	
XX		
OS	Homo sapiens.	
XX		
PN	W09932143-A1.	
XX		
PD	01-JUL-1999.	
XX		
PF	22-DEC-1998;	98WO-US27498.
XX		
PR	23-DEC-1997;	97US-0996744.
XX		
PA	(NUVA-) NUVAS LLC.	
XX		
PI	Dickinson CD, Houston LL;	
XX		
DR	WPI: 1999-405116/34.	
DR	N-PSDB: X78890.	
XX		
PT	New thrombogenic polypeptides used to, e.g. obliterate vasculative malformations	

PS Claim 30; Page 82-85; 97pp; English.
 XX
 CC This invention describes novel thrombogenic polypeptides which comprise a
 CC thrombogenic substructure and a context-dependent entity which recognizes
 CC desired biologically susceptible sites, e.g. tumour vascular endothelium.
 CC A novel context-dependent functional entity comprises a substructure with
 CC thrombogenic potential and one or more context-enhancing substructures
 CC having the ability to recognize desired biologically susceptible sites,
 CC where the entity imparts thrombogenic activity when positioned in the
 CC function-forming context at the biologically susceptible sites, and the
 CC entity has no thrombogenic activity absent a function-forming context at
 CC the biologically susceptible sites. The context-dependent functional
 CC entities impart thrombogenic activity only at biologically susceptible
 CC sites. They can be used to obliterate vasculature malformations or to
 CC selectively thrombose the vasculature of solid tumours. This sequence
 CC represents the human tissue factor protein Nuy125 which is used in the
 CC method of the invention.
 CC
 SQ
 XX Sequence 351 AA;
 Query Match 10.1%; Score 115.5; DB 20; Length 351;
 Best Local Similarity 26.0%; Pred. NO. 0.0012;
 Matches 61; Conservative 30; Mismatches 81; Indels 63; Gaps 15;
 QY 5 SPDYDESCTEFISLR--NFRSLTSMELKNHSIVPTHLLTYLTISKPEDIKVYKNCANT 62
 Db 139 spgctntvaaynlktksnfkllwepx-----pvngyvtvgstksqgdsk--skctyt 191
 QY 63 TRSFCDLDFDE-WRSTHEAVYVYLSGF-----SGNTTFPSCGHNFWLAIDMSFEPP- 111
 Db 192 ldtcedlidelvkdqkytlarvfsgpagnvestsgadepilysenpctpyltnlqpt 251
 QY 112 --EFEIVGTHNINWVKKP--SIVEEELQF-----DLSIVT--EEDSGEIVKHK 156
 Db 253 lqsfteqvg--tkvnytvdeertlvrrnmtflslidvfgkdlllycllywkssssg-----k 304
 QY 157 PEIKNGMSGNFTYIIDKLIPTNTVCVSYLEHSDQAVI-----KSPCLK 201

Db 305 kkatn.tneflidvdk--genycfsv-----qavipstrvnrkstdspvec 348

RESULT 10

ID R54236 standard; Protein; 263 AA.

AC R54236;

DT 08-SEP-1994 (first entry)

XX Human tissue factor mutant.

DE Tissue factor; Factor-VII; Factor-VIIA; Factor-X; plasma protein;

KW blood-clotting; coagulation; diagnostic; therapeutic; mutagenesis.

XX Homo sapiens.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Protein 1..263

FT W09407515-A.

PD 14-APR-1994.

PE 06-OCT-1993; 93WO-US09570.

PR 06-OCT-1992; 92US-0957985.

PA (SCRI) SCRIPPS RES INST.

PI Edgington TS, Ruf W;

DR WPI; 1994-135215/16.

XX Mutant human tissue factor protein - lacks factor VIIA activation

PT activity, useful in assays for plasma factor VIIA concn. and in

PT therapy to reduce factor VIIA dependent coagulation.

PS Claim 3; Page 91; 102pp; English.

CC Mutant human tissue factor proteins (given in R54236-43) bind

CC Factor-VII/VIIA and hydrolyze Factor-X when present in a complex

CC with VIIA, but cannot activate Factor-VII. The proteins have

CC amino acid substitutions in the 106-219 region of wild-type human

CC tissue factor (R54235), and were obtained by site-directed

CC mutagenesis of the wild-type gene (given in Q64219).

XX Sequence 263 AA;

Query Match 9.9%; Score 113.5; DB 15; Length 263;

Best Local Similarity 24.6%; Pred. No. 0.0012;

Matches 58; Conservative 26; Mismatches 65; Indels 87; Gaps 13;

Db 21 NFRSLSELKLNHSIVPHYTLTYIMSKPEDLVKVKNCANTTSFCDLDE-WRSTHEA 79

Db 18 nftlllewpk-----pvnqyvtvqistksqdkw--skcftltdccldelivadvkqt 70

QY 80 YVTVLEGF-----SGNTTLFSCSHNFWLAIDMSFEPP---EFETVGFTHNHNVMVK 127

Db 71 ylarvfyspagnvestsagsgeplyenspefcpyletnlgqptlgsfegvg--tkvntve 127

QY 128 FPSIVEEELQDLSLVIEQSEGIV-----KKHPEIKGNMNGNFTYIIDKLINNT 168

Db 128 -----edertlvrrnntflsrdvfqkdllytlryrkgsassgkktak 169

QY 169 -----YIIDKLINNTNVCVSYVLEHSDQAVI-----KSPDKCTLLPQGE 209

Db 170 tntneflid-vdkgenycfsv-----qavipstrvnrkstdspvecm---gqe 213

RESULT 11

ID R54243 standard; Protein; 263 AA.

AC R54243;

DT 08-SEP-1994 (first entry)

XX Human tissue factor mutant.

DE Tissue factor; Factor-VII; Factor-VIIA; Factor-X; plasma protein;

KW blood-clotting; coagulation; diagnostic; therapeutic; mutagenesis.

XX Homo sapiens.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Protein 1..263

FT W09407515-A.

PD 14-APR-1994.

PE 06-OCT-1993; 93WO-US09570.

PR 06-OCT-1992; 92US-0957985.

PA (SCRI) SCRIPPS RES INST.

PI Edgington TS, Ruf W;

DR WPI; 1994-135215/16.

XX Mutant human tissue factor protein - lacks factor VIIA activation

PT activity, useful in assays for plasma factor VIIA concn. and in

PT therapy to reduce factor VIIA dependent coagulation.

PS Claim 3; Page 91; 102pp; English.

CC Mutant human tissue factor proteins (given in R54236-43) bind

CC Factor-VII/VIIA and hydrolyze Factor-X when present in a complex

CC with VIIA, but cannot activate Factor-VII. The proteins have

CC amino acid substitutions in the 106-219 region of wild-type human

CC tissue factor (R54235), and were obtained by site-directed

CC mutagenesis of the wild-type gene (given in Q64219).

XX Sequence 263 AA;

Query Match 9.9%; Score 113.5; DB 15; Length 263;

Best Local Similarity 26.7%; Pred. No. 0.0012;

Matches 59; Conservative 25; Mismatches 80; Indels 57; Gaps 13;

Db 21 NFRSLSELKLNHSIVPHYTLTYIMSKPEDLVKVKNCANTTSFCDLDE-WRSTHEA 79

Db 18 nftlllewpk-----pvnqyvtvqistksqdkw--skcftltdccldelivadvkqt 70

QY 80 YVTVLEGF-----SGNTTLFSCSHNFWLAIDMSFEPP---EFETVGFTHNHNVMVK 127

Db 71 ylarvfyspagnvestsagsgeplyenspefcpyletnlgqptlgsfegvg--tkvntve 128

QY 128 FPSIVEEELQDLSLVIEQSEGIV-----KKHPEIKGNMNGNFTYIIDKLINNT 178

Db 129 derltvrrnntflgl-ldfrkgllytlrykssassgkktakn-tneflidvdk---ge 183

QY 179 NVCVSYVLEHSDQAVI-----KSPDKCTLLPQGE 209

Db 184 nycfsv-----qavipstrvnrkstdspvecm---gqe 213

ID	Y25404	standard; Protein: 266 AA.
XX	Y25404:	
AC	Y25404:	
XX		
DT	08-SEP-1999	(first entry)
XX		
DE	Human tissue factor clone NuV121 protein.	
XX		
KW	Tissue factor; human; thrombogenic; substructure; thrombose; tumour;	
KW	vasculative malformation; vascular endothelium; NuV121.	
XX		
OS	Homo sapiens.	
XX		
PN	WO932143-A1.	
XX		
PD	01-JUL-1999.	
XX		
PF	22-DEC-1998; 98WO-US27498.	
XX		
PR	23-DEC-1997; 97US-0996744.	
XX		
PA	(NUVA-) NUVAS LLC.	
XX		
FI	Dickinson CD, Houston LL;	
XX		
DR	WPI: 1999-405116/34.	
DR	N-PSDB; X78871.	
XX		
PT	New thrombogenic polypeptides used to, e.g. obliterate vasculative	
PT	malformations	
PS	Claim 30; Page 71-74; 97Pp; English.	
XX		
PS		
XX		
CC	This invention describes novel thrombogenic polypeptides which comprise a	
CC	thrombogenic substructure and a context-dependent entity which recognizes	
CC	desired biologically susceptible sites, e.g. tumour vascular endothelium.	
CC	A novel context-dependent functional entity comprises a substructure with	
CC	thrombogenic potential and one or more context-enhancing substructures	
CC	having the ability to recognize desired biologically susceptible sites,	
CC	where the entity imparts thrombogenic activity when positioned in the	
CC	function-forming-context at the biologically susceptible sites, and the	
CC	entity has no thrombogenic activity absent a function-forming-context at	
CC	the biologically susceptible sites. The context-dependent functional	
CC	entities impart thrombogenic activity only at biologically susceptible	
CC	sites. They can be used to obliterate vasculative malformations or to	
CC	selectively thrombose the vasculature of solid tumours. This sequence	
CC	represents the human tissue factor protein NuV121 which is used in the	
CC	method of the invention.	
XX		
XX		
Sequence	266 AA;	

Query Match	9.9%	Score 113.5;	DB 20;	Length 266;
Best Local Similarity	26.0%	Pred. No. 0.0013;		
Matches 61;	Conservative 29;	Mismatches 82;	Indels 63;	Gaps 15;
Oy	5	SPDYDESCFCRISLR--NFRSILSMELKNHSIVPTHLLTYTMSKPEDLKVKVNCANT	62	
Db	54	spgntntaaaynlkxskcnfklllewepk-----pvngyvtvgajstksqdkw--skfcyt	106	
Oy	63	TRSFCDLTDE-WRSTHEAVVTVLESGF-----SGNTTFSCSHNFWLAIDMSFEPP-	111	
Db	107	ltcedldldelvkdkqcyllarvfypagnavestsgsagepilyanpelfryletlqpt	166	
Oy	112	-EEFIEVFNNHINWKEP-SIVEEELQF-----DLSLVI--EEQEGIVKKHK	156	
Db	167	lqsfqgvy--ekvnvtvedertlvrnmtflslrdvfgkdllytllywksssg-----k	219	
Oy	157	PEIKNMSGNFYTIIDKLIPNTNCVSVYLEHSDQAVI-----KSPLEK	201	
Db	220	ktaktn-tnelfldwdk--genyfcfsv-----qavpstrvtmrktsdpsvc	263	

RESULT	13	
ID	Y25409	
AC	Y25409 standard; Protein; 276 AA.	
XX		
XX	Y25409;	
DT	08-SEP-1999 (first entry)	
XX		
DE	Human tissue factor clone NuV144 protein.	
XX		
XX	Tissue factor; human; thrombogenic; substructure; thrombose; tumour;	
KW	vasculative malformation; vascular endothelium; NuV144.	
XX		
OS	Homo sapiens.	
XX		
PN	WO932143-A1.	
XX		
PD	01-JUL-1999.	
XX		
PF	22-DEC-1998; 98WO-US27498.	
XX		
PR	23-DEC-1997; 97US-0996744.	
XX		
PA	(NUVA-) NUVAS LLC.	
XX		
PI	Dickinson CD, Houston LL;	
XX		
DR	WPI; 1999-405116/34.	
XX	N-PSDB; X78896.	
XX		
PT	New thrombogenic polypeptides used to, e.g. obliterate vasculative	
PT	malformations	
XX		
PS	Claim 30; Page 90-92; 97pp; English.	
XX		
CC	This invention describes novel thrombogenic polypeptides which comprise a	
CC	thrombogenic substructure and a context-dependent entity which recognizes	
CC	desired biologically susceptible sites, e.g. tumour vascular endothelium.	
CC	A novel context-dependent functional entity comprises a substructure with	
CC	thrombogenic potential and one or more context-enhancing substructures	
CC	having the ability to recognize desired biologically susceptible sites,	
CC	where the entity imparts thrombogenic activity when positioned in the	
CC	function-forming-context at the biologically susceptible sites, and the	
CC	entity has no thrombogenic activity absent a function-forming-context at	
CC	the biologically susceptible sites. The context-dependent functional	
CC	entities impart thrombogenic activity only at biologically susceptible	
CC	sites. They can be used to obliterate vasculative malformations or to	
CC	selectively thrombose the vasculature of solid tumours. This sequence	
CC	represents the human tissue factor protein NuV144 which is used in the	
CC	method of the invention.	

```

Query Match          9 9%  Score 113.5;  DB 20;  Length 276;
Best Local Similarity 26.0%;  Pred. NO. 0.0013;
Matches 61;  Conservative 29;  Mismatches 82;  Indels 63;  Gaps 15;

OY 5 SPDYDTDESCTEKISLR--NFRSILSMELKNHSIVPTHYLLLTITMSKPEDLTVKNCANT 62
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 spgtntvaaylltwksnfklilewepk----pvngyvtqatksqdwk--skcfylt 116

OY 63 TRSFEDLDE--WRSTHEAYVTVLEGF-----SGNTTSCSHNMLAIDMSEEP-- 111
   ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 ttdcedtdelcvkdkqgylarvfyspgnvestsagsberplyenspetrylethlgapt 176

OY 112 --EFTVIGFTNHINMVKFP--SIVVEELQF-----DLSLVI--EEQSEGIVAKKH 156
   ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 lqstqvgv--tkvavtvederlvrnmtflslrdgfgkdililylykxsssgs-----k 229

OY 157 PEIKNMSGNFYTIIDKLIPNTNCVSVYLHSDQAVI-----KPLK 201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


Dd 230 ktakun-lneflldvdk---genyofsv-----gavlpstvnrkstdspvec 273

RESULT 14
ID Y25408
XX Y25408 standard; Protein; 357 AA.
AC Y25408;
XX
DT 08-SEP-1999 (first entry)
XX
DE Human tissue factor clone NuVt129 protein.
XX
KW Tissue factor; human; thrombogenic; substructure; thrombose; tumour;
KW vasculative malformation; vascular endothelium; NuVt129.
XX
OS Homo sapiens.
XX
MO MO9932143-A1.
XX
PN 01-JUL-1999.
PD
XX
PR 22-DEC-1998; 98WO-US27498.
PF
XX
PR 23-DEC-1997; 97US-0996744.
XX
PA (NUVA-) NUVAS LLC.
XX
PI Dickinson CD, Houston LL;
XX
DR WPI; 1999-405116/34.
XX
N-PSDB; X78893.
XX
PT New thrombogenic polypeptides used to, e.g. obliterate vasculature
malformations
XX
PS

Claim 30; Page 85-88; 97pp; English.

xx This invention describes novel thrombogenic polypeptides which comprise a
CC thrombogenic substructure and a context-dependent entity which recognizes
CC desired biologically susceptible sites, e.g. tumour vascular endothelium.
CC A novel context-dependent functional entity comprises a substructure with
CC thrombogenic potential and one or more context-enhancing substructures
CC having the ability to recognize desired biologically susceptible sites,
CC where the entity imparts thrombogenic activity when positioned in the
CC function-forming context at the biologically susceptible sites, and the
CC entity has no thrombogenic activity absent a function-forming context at
CC the biologically susceptible sites. The context-dependent functional
CC entities impart thrombogenic activity only at biologically susceptible
CC sites. They can be used to obliterate vasculative malformations or to
CC selectively thrombose the vasculature of solid tumours. This sequence
CC represents the human tissue factor protein NuVt129 which is used in the
method of the invention.

SQ Sequence 357 AA;

OQuery Match 9.9%; Score 113.5; DB 20; Length 357;
Best local Similarity 26.0%; Pred. No. 0.0019;
Matches 61; Conservative 29; Mismatches 82; Indels 63; Gaps 15

OY 5 SPDYDESCTEFISLR--NFRSILSMELKNHSIVPTHYLTLTIMSKPEDLKVKMKCANT 62
|| : : : ||| | | | : : :
Db 145 spgtatvaagylalktskrtfkllwepk-----pvngyyvtqistksgdwk--skcft 197

OY 63 TRSFCDLIDE-WRSHEAVTVLEGF-----SGNTLFSCSHNEFLAIDMSFEPP 111
| : ||||| : : : : : | : : : :
Db 198 ldtcdlcldeivkvdkqtjlarvfaypagvestgsagsplyenapfeyletnlsgpt 257

OY 112 --EFEIYGTTNNINNVKKRP-SIVEEELQF-----DLSLVI--EEQGEGIVKRRK 156
| | | | : : | : : : | : : : | : : : | : : : | : : :
Db 258 lqsifeavg--tkvntlvvederltvirrntlflslrdvgkdilytllywkwsssg-----k 310

Query Match	Best Local Similarity	Score	Length
Matches 42: Conservative 33: Mismatches 82: Indels 20: Gaps 7:	9.8%; 23.7%;	112; 0.0048;	553;
21 NFRSLTSMSE----	LNKHSIVPTHYLLLTITMSKPEDLKVYKNCANTTRSECDLTDEWRS-	75	

Db 49 nmknvlgwtppeg1qg--vkvtctvqyfiyqkwlk-ksecrninrlycdlsaelsdy 104
QY 76 THEAYVTVLEGFSGNTTLFSCSHNFWLAIDMSFEPPEFEIYGFTNHNINWVKFPSIVEEE 135
Db 105 ehgyakvkaiwgtkcskwaesgrfypfletqigppevalttdeksisvvltapekwxkn 164
QY 136 LQFDLSIVIEE0SGEIVKHKHPEIKGNMSG-----NFTYIIDKLIPNTNVCVSV 184
Db 165 pe-dlpvsmqlysnl--kynvasvlntknsrtwsgvctnhtlvltwlepntlycvhv 218

Search completed: December 14, 2000, 10:27:22
Job time: 39 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 14, 2000, 10:26:47 ; Search time 38.96 Seconds
(without alignments)
1061.723 Million cell updates/sec

Title: US-09-166-298-26
Perfect score: 2377
Sequence: 1 ISYDSPDYTDESCTEFKISLR.....MHEALHNYTKSLSPGK 443

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues
Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_14:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_todent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1123	47.2	239	4	Q15467
2	831	35.0	437	11	Q91A4
3	516	21.7	513	11	Q35238
4	515	21.7	513	11	Q35664
5	510	21.5	247	11	Q35663
6	506	21.3	248	11	Q35983
7	288.5	12.1	384	4	Q9UP60
8	285	12.0	684	13	Q90544
9	233	9.8	508	13	Q9PVK0
10	229	9.6	508	13	Q9YHV9
11	190	8.0	509	11	Q9QX57
12	190	8.0	513	11	P97797
13	188	7.9	509	11	Q08907
14	185	7.8	268	13	Q90524
15	180.5	7.6	506	6	Q46632
16	178	7.5	506	6	Q46631
17	176.5	7.4	259	13	Q90530
18	176.5	7.4	509	11	Q9WTA4
19	171.5	7.2	257	13	Q90536

20	170	7.2	237	13	Q90545	Q90545 ginglymosto
21	167.5	7.0	252	13	Q90568	Q90568 ginglymosto
22	166.5	7.0	267	13	Q90529	Q90529 ginglymosto
23	164.5	6.9	398	4	Q00241	Q00241 homo sapien
24	162	6.8	261	7	Q19363	Q19363 sus scrofa
25	161.5	6.8	397	4	Q9YAV0	Q9YAV0 homo sapien
26	156	6.6	418	11	Q70426	Q70426 ratu
27	156	6.6	509	11	P97710	P97710 ratu
28	155	6.5	261	7	Q62868	Q62868 sus scrofa
29	154.5	6.5	429	4	Q43799	Q43799 homo sapien
30	153	6.4	324	4	Q9YU9	Q9YU9 homo sapien
31	152.5	6.4	504	4	Q9UT6	Q9UT6 homo sapien
32	151	6.4	509	11	Q9QW15	Q9QW15 ratu
33	147.5	6.2	248	7	Q98044	Q98044 aulonocara
34	147	6.2	503	4	P78324	P78324 homo sapien
35	146.5	6.2	261	7	Q98263	Q98263 sus scrofa
36	144	6.1	214	11	Q9R1A5	Q9R1A5 mus musculu
37	143	6.0	260	7	P79551	P79551 homo sapien
38	142.5	6.0	183	7	Q29922	Q29922 homo sapien
39	142.5	6.0	261	7	Q30099	Q30099 homo sapien
40	142	6.0	183	7	Q30102	Q30102 homo sapien
41	141.5	6.0	183	7	Q30090	Q30090 homo sapien
42	141.5	6.0	229	7	Q30075	Q30075 homo sapien
43	141	5.9	261	7	Q30091	Q30091 homo sapien
44	140.5	5.9	188	7	Q95466	Q95466 homo sapien
45	140.5	5.9	238	7	Q31467	Q31467 morone saxa

ALIGNMENTS

RESULT 1
ID Q15467 PRELIMINARY; PRT: 239 AA.

AC Q15467; 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE SOLUBLE IFN ALPHA/BETA RECEPTOR PRECURSOR.
GN IFNABR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE; 95279874.
RA Novick D., Cohen B., Tal N., Rubinstein M.;
RT "Soluble and membrane-anchored forms of the human IFN-alpha/Beta
receptor";
RL J. Leukoc. Biol. 57:712-718(1995).
CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
DR EMBL; X89614; CA61940.1; -;
DR INTERPRO; IPR000282; -;
KW Receptor; Signal.
FT SIGNAL 1..26 POTENTIAL.
FT CHAIN 27..239 SOLUBLE IFN ALPHA/BETA RECEPTOR.
SQ SEQUENCE 239 AA; 27336 MW; 138DC54AA1CIA1A2 CAC64;

Query Match 47.2%; Score 1123; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 6.4e-85;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISYDSPDYTDESCTEFKISLRNRSILSWELKXHSIVPHYTLTYITMSKPEDLKXVKNCA 60
DB 27 ISYDSPDYTDESCTEFKISLRNRSILSWELKXHSIVPHYTLTYITMSKPEDLKXVKNCA 86
QY 61 NTRRSFCDLTDEMRSTHEAYVTVLEGFSGNTTLESCSHNFWLAIDMSFPPFEIIVGFTN 120
DB 87 NTRRSFCDLTDEMRSTHEAYVTVLEGFSGNTTLESCSHNFWLAIDMSFPPFEIIVGFTN 146
QY 121 HINWVAKPEPSIVEEDLPDLSLVIEOSEGIYKHKRPEIKMGSGNFTYIIDKLIPNTNY 180

```
Db 147 HINWNAKFPIVEEELQFDLSLVEOSEGIVKHKKEIKGNMGNFTYIIDKLIPMTNY 206
QY 181 CVAHYLEHSDQAVIKSPKLTLLPQGESE 211
Db 207 CVAHYLEHSDQAVIKSPKLTLLPQGESE 237

RESULT 2
Q9RI44
ID 035238 PRELIMINARY; PRT: 437 AA.
AC 035238:
DT 01-JAN-1998 (TREMblrel. 13, Created)
DT 01-JAN-1998 (TREMblrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMblrel. 14, last annotation update)
DE GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]

RN
SEQUENCE FROM N.A.
RX MEDLINE: 97442458.
RA Owczarek C.M., Hwang S.Y., Holland K.A., Gulluyan L.M., Tavarie M.,
RA Weaver B., Reich N.C., Kola I., Hertzog P.J.;
RT "Cloning and characterization of soluble and transmembrane isoforms of
RT a novel component of the murine type I interferon receptor, IFNAR 2.";
RL J. Biol. Chem. 272:23865-23870(1997).
DR EMBL: AF013274; AAC53351.1; -.
DR MGD: MGI:1098243; Ifnar2.
DR INTERPRO: IPR000282; -.
KM Signal.
FT SIGNAL.
SQ SEQUENCE 513 AA; 56623 MW; 602FC47D057EC372 CRC64;

Query Match 21.7%; Score 516; DB 11; Length 513;
Best Local Similarity 31.9%; Pred. No. 1.7e-34;
Matches 152; Conservative 73; Mismatches 146; Indels 106; Gaps 18;

QY 8 YTDSECTFKISLRNFRSILSWELKNHSIVPTHYLLTYTINSKPEDLVKVKNCANTRSFC 67
Db 34 YPDEPCTINITIRNSRLILSWELKNKSGPRANTYLTWTVMKSDNLTKVKNCSPTTSSC 93
QY 68 DLNDEMSTHEAY-VTVLEFGSNTTLFSCSNFMFLAIDMSFEPPEPEIYGFTHINMV 126
Db 94 DVTQKLEGMESYVAIVYVHRGDLVCRCS-DYIVPANAPLEPEPEIYGFTHINVTM 152
QY 127 KFP-----SYEEELQFDLSLVEOSEGIVKHKKEIKGNMGNFTYIIDKLIPNTYCV 182
Db 153 EEPVTSKIIQEKMKTPPEYKLEQIGSVRKHKPKV-NNTGNTFTVLRDLRLKTYCV 211
QY 183 SVYLEHSDQAVIKSPKLTLLPQGESESAESA--DKTHTCP----- 224
Db 212 SLVF---DDPAIKSPKLCYLVQPGESGLSESAIVGITTSCLVVMFVSTIVLKKITGY 268
QY 225 -CPAPELLGSPVLF-----PPKPKDTLMISRTPEVTCV---VVDVSHEDP 267
Db 269 ICLKDNL---PNVLNFRHFLTWIIPERSPEAIDRLIEPTNKKRLMNYDEGSDSDE 325
QY 268 EVKKNWVVDQEVINAKTKPREBOYNSTRVSVLYLVLDHDMVNGKEYKCVSKALPAP 327
Db 326 EVP-TASVGYTMHETLGRKPLQOTSDFS--ASPEDPLHEE-----DSG 365
QY 328 IEKTSKAKGPRPOVYTLTPRSREMTKNQVSLTCLYKGYPSDIAVEMESNGPENNY 387
Db 366 AEEDDEGAGAGAPELPT-----EAGAGPSE-----DPTGPT 398
QY 388 KTPPVLDSDGSFELYSLKLVKSRMOQ-----NVFSCSVMHBLNHNHYTKSL 439
Db 399 ERRKSVLED--SFRENSSMD-----EPGDIIIFVSLNSVFLVLDHEDASFTLSL 449

RESULT 4
Q35664
ID 035664 PRELIMINARY; PRT: 513 AA.
AC 035664:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-JUN-2000 (TREMblrel. 14, last annotation update)
DE TYPE I INTERFERON RECEPTOR SUBUNIT PRECURSOR.
GN IFNAR2 OR IFNAR2C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]

RN
SEQUENCE FROM N.A.
RX SPRAIN-C57 BLACK/6; TISSUE-BRAIN;
RX MEDLINE: 97464076.
RA Kim S.H., Cohen B., Novick D., Rubinstein M.;
RT "Mammalian type I interferon receptors consists of two subunits:
RT IFNAR1 and IFNAR2.";
RL Gene 196:279-286(1997).
```

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QY 201 CTLPLPGQESASADKTHT---CP--CPAPELLGSPVLFPPPKPKDTLMISRTP 253
Db 195 CNAHNP-----STKYVKKTIYPRDCGKPCCTIYPEV---SSVFIFPKPRDVLTLTPR 247
QY 254 EYTCVVVDVSHEDPEVKFNMYVDQGVENNAKTKPREBOYNSTRVSVLYLVLDHDMVNG 313
Db 248 KVCVVVDISKDPEVQFSNFVDVEVHTAQTQPREQFNSTRFSVELRIMHDMVNGK 307
QY 314 EYCKCKSNKALPAPIETKTSKAKGQPREPOVYTLTPRSREMTKNQVSLTCLYKGYPSDI 373
Db 308 EFCRCRVNSAFAFPARIEKTIKTKGRPKAPQVYTLTPRPEQMAKDKVSLTGMITDFPEDI 367
QY 374 AVEMESNGPENNYKTPPVLDSDGSFELYSLKLVKSRMOQGVNFCSVMHBLNHNHYT 433
Db 368 TVEMQWNGQPAENKKNPTIMDTGSGYVYSKLVNOKSNMEAGNTFCVSLHGLNHNHT 427
QY 434 OKSLSLSPGK 443
Db 428 EKNLSHSPGK 437
```

```
Query Match 35.0%; Score 831; DB 11; Length 437;
Best Local Similarity 59.2%; Pred. No. 1.6e-60;
Matches 148; Conservative 43; Mismatches 45; Indels 14; Gaps 4;

QY 201 CTLPLPGQESASADKTHT---CP--CPAPELLGSPVLFPPPKPKDTLMISRTP 253
Db 195 CNAHNP-----STKYVKKTIYPRDCGKPCCTIYPEV---SSVFIFPKPRDVLTLTPR 247
QY 254 EYTCVVVDVSHEDPEVKFNMYVDQGVENNAKTKPREBOYNSTRVSVLYLVLDHDMVNG 313
Db 248 KVCVVVDISKDPEVQFSNFVDVEVHTAQTQPREQFNSTRFSVELRIMHDMVNGK 307
QY 314 EYCKCKSNKALPAPIETKTSKAKGQPREPOVYTLTPRSREMTKNQVSLTCLYKGYPSDI 373
Db 308 EFCRCRVNSAFAFPARIEKTIKTKGRPKAPQVYTLTPRPEQMAKDKVSLTGMITDFPEDI 367
QY 374 AVEMESNGPENNYKTPPVLDSDGSFELYSLKLVKSRMOQGVNFCSVMHBLNHNHYT 433
Db 368 TVEMQWNGQPAENKKNPTIMDTGSGYVYSKLVNOKSNMEAGNTFCVSLHGLNHNHT 427
QY 434 OKSLSLSPGK 443
Db 428 EKNLSHSPGK 437

RESULT 3
Q35238
ID 035238 PRELIMINARY; PRT: 513 AA.
AC 035238:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-JUN-2000 (TREMblrel. 14, last annotation update)
DE TYPE I INTERFERON RECEPTOR PRECURSOR.
GN IFNAR2 OR IFNAR2C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
```

DR EMBL: Y09865; CAA70992.1; -
 DR MGD: MGI:1098243; Ifnar2.
 DR INTERPRO: IPR000282; -
 KW Signal.
 FT SIGNAL.
 SO SEQUENCE 513 AA: 56568 MW: 601BFE6CEFA8CB73 CRC64;

Query Match 21.7%; Score 515; DB 11; Length 513;
 Best Local Similarity 47.7%; Pred. No. 2,1e-34;
 Matches 102; Conservative 46; Mismatches 56; Indels 10; Gaps 5;

QY 8 YTDSCFKISLRNRSILSMELKNSIVPTHTLLYTMSKPEDLKVKVNCANTTRSC 67
 DB 34 YPDECTINITIRNSRLISWELKNSGPRANYTLMYTMSKDEMLTKVKNCSDTTKSSC 93
 QY 68 DLTDMRSTHEAY-VTVLEGFSGNTLTFSCSHNFMALIDMSPEPEFVGTNNHINWV 126
 DB 94 DVTDKWLMGEMESYVAIVHGRDLTVCRCS-DYIVPANAPLPEPEFVGTNNHINWV 152
 QY 127 KFP----SIVEBELQFDLSVIEQSEGIYVKKHKEIKGNSGNFTYIIDKLIPNTNCV 182
 DB 153 EEPPTSQLIDKMKTTFFVKEQIGDSYRKKEPKV-NNVYGNFTFVLRDLPTKNTCV 211
 QY 183 SVLEHSDQAVIKSPKCTLLPQGESESA 216
 DB 212 SLVF---DDPAIKSPKCIYVLPQGESESA 242

RESULT 5
 ID 035663 PRELIMINARY; PRT; 247 AA.
 AC 035663;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE SOLUBLE TYPE I INTERFERON RECEPTOR SUBUNIT PRECURSOR.
 GN IFNAR2 OR IFNAR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57 BLACK/6; TISSUE=BRAIN;
 RX MEDLINE: 97464076.
 RA Kim S.H., Cohen B., Novick D., Rubinstein M.;
 RT "Mammalian type I interferon receptors consists of two subunits:
 RT IFNAR1 and IFNAR2."
 RL Gene 196:279-286(1997).
 DR EMBL: Y09864; CAA70991.1; -
 DR MGD: MGI:1098243; Ifnar2.
 DR INTERPRO: IPR000282; -
 KW Signal.
 FT SIGNAL.
 SO SEQUENCE 247 AA: 27609 MW: 4957A16710C2D2D1 CRC64;

Query Match 21.5%; Score 510; DB 11; Length 247;
 Best Local Similarity 47.8%; Pred. No. 2e-34;
 Matches 100; Conservative 45; Mismatches 54; Indels 10; Gaps 5;

QY 8 YTDSCFKISLRNRSILSMELKNSIVPTHTLLYTMSKPEDLKVKVNCANTTRSC 67
 DB 34 YPDECTINITIRNSRLISWELKNSGPRANYTLMYTMSKDEMLTKVKNCSDTTKSSC 93
 QY 68 DLTDMRSTHEAY-VTVLEGFSGNTLTFSCSHNFMALIDMSPEPEFVGTNNHINWV 126
 DB 94 DVTDKWLMGEMESYVAIVHGRDLTVCRCS-DYIVPANAPLPEPEFVGTNNHINWV 152
 QY 127 KFP----SIVEBELQFDLSVIEQSEGIYVKKHKEIKGNSGNFTYIIDKLIPNTNCV 182
 DB 153 EEPPTSQLIDKMKTTFFVKEQIGDSYRKKEPKV-NNVYGNFTFVLRDLPTKNTCV 211

QY 183 SVLEHSDQAVIKSPKCTLLPQGESE 211
 DB 212 SLVF---DDPAIKSPKCIYVLPQGESE 237

RESULT 6
 ID 035983 PRELIMINARY; PRT; 248 AA.
 AC 035983;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE TYPE I INTERFERON RECEPTOR SOLUBLE ISOFORM PRECURSOR.
 GN IFNAR2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 97442458.
 RA Owczarek C.M., Hwang S.Y., Holland K.A., Gulluyan L.M., Tavaría M.,
 RA Weaver B., Reich N.C., Kola I., Hertzog P.J.;
 RT "Cloning and characterization of soluble and transmembrane isoforms of
 RT a novel component of the murine type I interferon receptor, IFNAR 2."
 RL J. Biol. Chem. 272:23865-23870(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Owczarek C.M., Hwang S.Y., Holland K.A., Gulluyan L.M., Tavaría M.,
 RA Weaver B., Reich N., Kola I., Hertzog P.J.;
 RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57 BLACK/6; TISSUE=BRAIN;
 RX MEDLINE: 97464076.
 RA Kim S.H., Cohen B., Novick D., Rubinstein M.;
 RT "Mammalian type I interferon receptors consists of two subunits:
 RT IFNAR1 and IFNAR2."
 RL Gene 196:279-286(1997).
 DR EMBL: AF013486; AAC53352.1; -
 DR EMBL: Y09813; CAA70943.1; -
 DR MGD: MGI:1098243; Ifnar2.
 DR INTERPRO: IPR000282; -
 KW Signal.
 FT SIGNAL.
 FT CHAIN 28 248 TYPE I INTERFERON RECEPTOR SOLUBLE
 FT ISOFORM.
 SO SEQUENCE 248 AA: 27755 MW: 47D6008193F7BC3C CRC64;

Query Match 21.3%; Score 506; DB 11; Length 248;
 Best Local Similarity 47.4%; Pred. No. 4.4e-34;
 Matches 100; Conservative 45; Mismatches 56; Indels 10; Gaps 5;

QY 8 YTDSCFKISLRNRSILSMELKNSIVPTHTLLYTMSKPEDLKVKVNCANTTRSC 67
 DB 34 YPDECTINITIRNSRLISWELKNSGPRANYTLMYTMSKDEMLTKVKNCSDTTKSSC 93
 QY 68 DLTDMRSTHEAY-VTVLEGFSGNTLTFSCSHNFMALIDMSPEPEFVGTNNHINWV 126
 DB 94 DVTDKWLMGEMESYVAIVHGRDLTVCRCS-DYIVPANAPLPEPEFVGTNNHINWV 152
 QY 127 KFP----SIVEBELQFDLSVIEQSEGIYVKKHKEIKGNSGNFTYIIDKLIPNTNCV 182
 DB 153 EEPPTSQLIDKMKTTFFVKEQIGDSYRKKEPKV-NNVYGNFTFVLRDLPTKNTCV 211
 QY 183 SVLEHSDQAVIKSPKCTLLPQGESESA 213
 DB 212 SLVF---DDPAIKSPKCIYVLPQGESESA 239

RESULT 7
 ID 090P60 PRELIMINARY; PRT; 384 AA.
 Q90P60

997797	PRELIMINARY. PRT. 513 AA.
ID	P97797. p97796; 035924; 086555; 086556;
AC	01-NOV-1998 (TREMBLrel. 08, Created)
DT	01-NOV-1998 (TREMBLrel. 08, last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, last annotation update)
DE	PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR (P84) (SHP SUBSTRATE-1) (INHIBITOR RECEPTOR SHPS-1) (SHPS-1) (SHPS1).
GN	PTPNS1 OR P84 OR SHPS-1 OR SHPS1 OR BTT.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RX	MEDLINE: 97223399.
RA	Yamao T., Matozaki T., Amano K., Matsuda Y., Takahashi N., Ochi F., Fujitaka Y., Kasuga M.:
RT	"Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal localization of genes."
RL	Biochem. Biophys. Res. Commun. 231:61-67(1997).
RN	[2]
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 32-53: 422-424 AND 429-433.
RC	STRAIN=BA1B/C. TISSUE=CEREBELLUM, AND BRAIN:
RA	Comu S., Weng W., Olinisky S., Ishwad P., Mi Z., Hempel J., Watkins S., Lagenaur C.F., Narayanan V.:
RT	"The murine P84 neural adhesion molecule is SHPS-1, a member of the phosphatase-binding protein family."
RL	J. Neurosci. 17:8702-8710(1997).
RN	[3]
RP	SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC	STRAIN=C57BL/6; TISSUE=FETAL THYMUS;
RX	MEDLINE: 98380500.
RA	Veillelle A., Thibaudau E., Latour S.:
RT	"High expression of inhibitory receptor SHPS-1 and its association with protein tyrosine phosphatase SHP-1 in macrophages."
RL	J. Biol. Chem. 273:22719-22728(1998).
RN	[4]
RP	SEQUENCE FROM N.A.
RC	STRAIN=129SV. TISSUE=LIVER:
RA	Sano S., Ohnishi H., Kubota M.:
RT	"Gene structure of mouse B17/SHPS-1."
RL	Biochem. J. 344:667-675(1999).
RN	[5]
RP	FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX	MEDLINE: 90152134.
RA	Chuang W., Lagenaur C.F.:
RT	"Central nervous system antigen P84 can serve as a substrate for neurite outgrowth."
RL	Dev. Biol. 137:219-232(1990).
CC	-1- FUNCTION: BINDS TO THE SH2 DOMAINS OF PROTEIN-TYROSINE PHOSPHATASE 2C (SHP-2) AFTER TYROSINE PHOSPHORYLATION INDUCED BY VARIOUS MITOGENS AND CELL ADHESION. PROTEIN SUPPORTS ADHESION OF CEREBELLAR NEURONS, NEURITE OUTGROWTH AND GLIAL CELL ATTACHMENT. MAY PLAY A KEY ROLE IN INTRACELLULAR SIGNALING DURING SYNAPTogenesis AND IN SYNAPTIC FUNCTION. MAY ACT AS A DOCKING PROTEIN AND INDUCE TRANSLLOCATION OF SHP-2 FROM THE CYTOSOL TO THE PLASMA MEMBRANE. TYROSINE PHOSPHORYLATED PTPNS1 FROM MACROPHAGES PRIMARILY ASSOCIATES WITH SHP-1.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-1- ALTERNATIVE PRODUCTS: THREE FORMS; ISOFORMS 1 (SHOWN HERE), 2 AND SMALL, ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN THE CEREBRAL CORTEX, CEREBELLUM, SPINAL CORD, SPLEEN AND MACROPHAGES AND AT MUCH LOWER LEVEL IN THE KIDNEY, HEART, LIVER AND THYMUS. WITHIN THE CEREBELLUM, EXPRESSION IS DETECTED IN THE SYNAPTIC GLOMERULI, GRANULE CELL BODIES, GOLGI EPITHELIAL CELLS, OLFACTORY BULB, NEURONS IN THE HIPPOCAMPUS AND THE DENTATE GYRUS. IN THE EYE, EXPRESSION IS FIRST SEEN IN THE INNER PLEXIFORM AND OPTIC FIBER LAYERS. LATER IN DEVELOPMENT EXPRESSION IS ALSO SEEN IN THE OUTER PLEXIFORM, RETINA AND OUTER SEGMENTS OF THE PHOTORECEPTOR LAYER.
CC	-1- DEVELOPMENTAL STAGE: EXPRESSED TO THE FLOOR PLATE REGION OF THE VENTRAL EXPRESSION IS RESTRICTED TO THE EMBRYO FROM DAY 7, WHEN
CC	NEURAXIS. WIDESPREAD EXPRESSION IN A VARIETY OF CNS REGIONS BEGINS 2-5 DAYS AFTER BIRTH.
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS TWO C1-LIKE AND ONE V-LIKE DOMAINS.
CC	EMBL: D87968; BA13521.1; -
DR	EMBL: D87967; BA13520.1; -
DR	EMBL: U88694; AAB92591.1; -
DR	EMBL: AF072543; AAC2486.1; -
DR	EMBL: AF072544; AAC24887.1; -
DR	EMBL: AB024507; BAA89290.1; -
DR	EMBL: AB024500; BAA89290.1; -
DR	EMBL: AB024501; BAA89290.1; JOINED.
DR	EMBL: AB024502; BAA89290.1; JOINED.
DR	EMBL: AB024503; BAA89290.1; JOINED.
DR	EMBL: AB024504; BAA89290.1; JOINED.
DR	EMBL: AB024505; BAA89290.1; JOINED.
DR	EMBL: AB024506; BAA89290.1; JOINED.
DR	MGI:108563; Ptpns1.
DR	INTERPRO: IPR000495; -
DR	INTERPRO: IPR003006; -
DR	PFAM: PF00047; 19; 3.
DR	PROSITE: PS00290; IG_MHC; UNKNOWN 1.
KW	Signal. Transmembrane. Alternative splicing; Immunoglobulin domain; Glycoprotein; SH3-binding; Phosphorylation.
FT	CHAIN 1 31
FT	32 513
FT	DOMAIN 32 373
FT	TRANSMEM 374 394
FT	DOMAIN 395 513
FT	DOMAIN 51 124
FT	DOMAIN 167 234
FT	DOMAIN 270 336
FT	DOMAIN 440 443
FT	DOMAIN 450 456
FT	DOMAIN 464 467
FT	DOMAIN 481 484
FT	DOMAIN 505 508
FT	MOD_RES 423 423
FT	MOD_RES 440 440
FT	MOD_RES 464 464
FT	MOD_RES 481 481
FT	MOD_RES 505 505
FT	MOD_RES 505 505
FT	CARBOHYD 54 54
FT	CARBOHYD 92 92
FT	CARBOHYD 168 168
FT	CARBOHYD 180 180
FT	CARBOHYD 205 205
FT	CARBOHYD 209 209
FT	CARBOHYD 246 246
FT	CARBOHYD 271 271
FT	CARBOHYD 293 293
FT	CARBOHYD 302 302
FT	CARBOHYD 312 312
FT	CARBOHYD 320 320
FT	CARBOHYD 345 345
FT	CARBOHYD 367 367
FT	VARSPPLIC 147 364
FT	VARSPPLIC 425 428
FT	CONFLICT 10 10
FT	CONFLICT 29 29
FT	CONFLICT 67 67
FT	CONFLICT 74 74
FT	CONFLICT 83 83
FT	CONFLICT 86 87
FT	CONFLICT 90 90
FT	CONFLICT 91 91
FT	CONFLICT 96 96
FT	CONFLICT 114 114

Db 114 LEEEDMIYVGGTGVNPGIPLSPIVSLHSATSEQRANGFVQLVCLISGYYPENIA 173
QY 375 VEMESNGQP-ENNYKTPPYLSDSGSEFFLYSKLTVDKSRMOQGVNFCSVHHEALHNHYT 433
Db 174 VSMQKNKTITSGPATISPYKTSNDSCASLKLKVPLOEMSRGSGVSCQVSHSATSSNOR 233
QY 434 OKSLSLIS 440
Db 234 KEIRSTS 240

RESULT 15

ID 046632 PRELIMINARY; PRT; 506 AA.
AC 046632;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MYD-1 ANTIGEN PRECURSOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE; 98143722.
RA Brooke G.P., Parsons K.R., Howard C.J.;
RT "Cloning of two members of the SIRP alpha family of protein tyrosine
phosphatase binding proteins in cattle that are expressed on monocytes
RT and a subpopulation of dendritic cells and which mediate binding to
RT CD4⁺ T cells.";
RL Eur. J. Immunol. 28:1-11(1998).
DR EMBL; Y11045; CAA71942.1; -.
DR INTERPRO: IPR003006; -.
DR PIRAM: PF00047; 1g; 3.
KW Signal.
FT SIGNAL. 1 26 POTENTIAL.
FT CHAIN 27 506 MYD-1 ANTIGEN.
SQ SEQUENCE 506 AA; 55117 MW; ACDDDEA9C9708A82 CRC64;

Query Match 7.6%; Score 180.5; DB 6; Length 506;
Best Local Similarity 25.6%; Pred. No. 7.3e-07;
Matches 62; Conservative 39; Mismatches 116; Indels 25; Gaps 7;

QY 201 CTLLPQGESE-SAESADKTH-TCPCPAPELIGGSPVFLFPPKPKDTLMISRPETCV 258
Db 121 CVKFPQKGEHDVEFKSGPGTHLVNAKFPSPVSGPTV-----RATPEQTVN 167
QY 259 VVDVSH--EDPEVKFMWYVDGVEVHNAKTRPREQVNSTYRVVSVLVLHODWLNKREYK 316
Db 168 FTCTSHGFSPRNISLWFKNGNELSASQTSVPDEDDNVSYSTSTKVLATGDVHSQVI 227
QY 317 CKYSNKAALPA-PIEKTISAKAGPREPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIA 374
Db 228 CEVAHYTLGGPPLRGANLSEITIRVPP--TLEITRSPSAGNOVNVTCQVKNKFYPRHLQ 284
QY 375 VEMESNGQPENNYKTPPYLSDSGSEFFLYSKLTVDKSRMOQGVNFCSVHHEALHNH 431
Db 285 LITWLENGNMSRTAASVLYENKDGTFNQTSWLIVNSSAHREAVVLTICQVEHROPAPAVSKN 344
QY 432 YT 433
Db 345 HT 346

Search completed: December 14, 2000, 10:30:22
Job time: 215 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 14, 2000, 10:27:32 ; Search time 16.07 Seconds
(without alignments)
880.705 Million cell updates/sec

Title: US-09-166-298-26
2377

Perfect score: 1 ISYDSPDYDESCFEKISLR.....MHEALHNHYTKSLSPGK 443

Sequence: BLOSUM62
Gapop 10.0 , Gapext 0.5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues
Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwlssProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1244	52.3	330	1	GCL_HUMAN
2	1160	48.8	326	1	GC2_HUMAN
3	1153.5	48.5	327	1	GC4_HUMAN
4	1153	48.5	290	1	GC3_HUMAN
5	1144	48.1	515	1	INR2_HUMAN
6	932.5	39.2	323	1	GC_RABIT
7	888.5	37.4	328	1	CC2_CAVPO
8	857	36.1	329	1	GC3_MOUSE
9	846	35.6	398	1	GC3_MOUSE
10	842.5	35.4	333	1	GC1_RAT
11	826	34.7	326	1	GCL_RAT
12	825.5	34.7	324	1	GCL_MOUSE
13	822.5	34.6	329	1	CC2_RAT
14	820.5	34.5	333	1	GC1_MOUSE
15	816	34.3	330	1	GCAB_MOUSE
16	811	34.1	335	1	GCAB_MOUSE
17	802	34.1	399	1	GCAM_MOUSE
18	802	33.7	332	1	GCA_RAT
19	786	33.1	336	1	GCB_MOUSE
20	781	32.9	405	1	GCB_MOUSE
21	722	30.4	536	1	INR2_BOVIN
22	688.5	29.0	536	1	INR2_SHEEP
23	374.5	15.8	429	1	EPC_RAT
24	365	15.4	454	1	MUC_HUMAN
25	365	15.4	458	1	MUC_RABIT
26	363.5	15.3	421	1	EPC_MOUSE
27	362.5	15.3	421	1	MUCB_HUMAN
28	358	15.1	455	1	MUC_MOUSE
29	355	14.9	479	1	MUCM_RABIT
30	354	14.9	428	1	EPC_HUMAN
31	348	14.6	457	1	MUC_SUNMU
32	348	14.6	476	1	MUC_MOUSE
33	343	14.4	450	1	MUC_CANFA

34	333	14.0	454	1	MUC_MESAU	P06337 mesocricetu
35	311	13.1	438	1	HVC2_HETER	P23085 heterodontu
36	302.5	12.7	299	1	ALC_RABIT	P01879 oryctolagus
37	295	12.4	438	1	HVC3_HETER	P23087 heterodontu
38	288.5	12.1	353	1	ALC1_HUMAN	P01876 heterodontu
39	288.5	12.1	466	1	MUC_CHICK	P01875 homo sapien
40	286	12.0	461	1	HVCM_HETER	P23088 heterodontu
41	285.5	12.0	370	1	HVC1_HETER	P23088 heterodontu
42	284.5	12.0	353	1	ALC1_GORGO	P20758 gorilla gor
43	284	11.9	393	1	HVC3_HETER	P23086 heterodontu
44	278	11.7	481	1	MUCM_ICTPU	P23735 ictalurus p
45	275.5	11.6	340	1	ALC2_HUMAN	P01877 homo sapien

ALIGNMENTS

RESULT 1	ID	GCL_HUMAN	STANDARD:	PRT:	330 AA.
AC	P01857				
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	15-JUL-1999	(Rel. 38, Last annotation update)			
DE	IG GAMMA-1 CHAIN C REGION.				
GN	IGHG1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 82274238.				
RA	Ellison J.W., Berson B.J., Hood L.E.;				
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";				
RL	Nucleic Acids Res. 10:4071-4079(1982).				
RN	[2]				
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).				
RX	MEDLINE: 71064024.				
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,				
RT	Maxdal M.J., Edelman G.M.;				
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino				
RN	acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";				
RL	Biochemistry 9:3161-3170(1970).				
RN	[3]				
RP	SEQUENCE OF 136-329 (EU).				
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,				
RT	Edelman G.M.;				
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino				
RN	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";				
RL	Biochemistry 9:3171-3181(1970).				
RN	[4]				
RP	SEQUENCE (MYELOMA PROTEIN NIE).				
RX	MEDLINE: 77070269.				
RA	Postnig H., Hilschmann N.;				
RT	"The rule of antibody structure. The primary structure of a				
RL	monoclonal IgG1 immunoglobulin (myeloma protein Nie). II. The				
RN	tryptophan residues of the H-chain, alignment of the tryptic				
RL	peptides and discussion of the complete structure.";				
RN	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).				
RN	[5]				
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.				
RX	MEDLINE: 832869131.				
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;				
RT	"Three-dimensional structure determination of antibodies. Primary				
RL	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";				
RN	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).				
RN	[6]				
RP	DISULFIDE BONDS.				
RX	MEDLINE: 71064027.				
RA	Gall W.E., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. X.				
RL	Intrachain disulfide bonds.";				

RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE: 77070267.
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.:
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nle). I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE: 81208100.
RA Deisenhofer J.:
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from *Staphylococcus*
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
CC MARKER & THE GIM (NON-1) MARKERS.
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35, 116, 198, 269 & 272.
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198, 267&272.
CC -----
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CC -----
DR EMBL: J00228; AAC82527.1; ALT_INIT.
DR PIR: A02146; GHNU.
DR PDB: 1FC1; 15-JUL-92.
DR PDB: 1FC2; 15-JUL-92.
DR MIM: 147100; -
DR INTERPRO: IPR000495; -
DR INTERPRO: IPR003006; -
DR PEFAM: PFO0047; 19; 3.
DR PROSITE: PS00290; IG_MHC; 2.
KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KM 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 223
FT DOMAIN 224 330
FT DISULFID 27 83
FT DISULFID 103 103
FT DISULFID 109 109
FT DISULFID 112 112
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT MOD_RES 330 330
FT STRAND 123 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164

FT STRAND 165 166
FT STRAND 175 178
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT STRAND 238 240
FT HELIX 241 242
FT TURN 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SO SEQUENCE 330 AA: 36106 MW: 370DE106C2FA33D CRC64:

Query Match 52.3%; Score 1244; DB 1; Length 330;
Best Local Similarity 68.7%; Pred. No. 1,4e-81;
Matches 246; Conservative 19; Mismatches 45; Indels 48; Gaps 6;

QY 88 SGNVTLFSCNHNFWLAIDMSFEP--PEFEIVGFNTHINWVKKPSVIEEELDFLSLVIE 145
DB 19 SCGFAALGCG-----LVNDYFPEPYTVSWNSGALTSVHT---FPAVQSSGLYSLSVVT 70
QY 146 EOSEGIVKKHKPEIKGMSGNFTYIIDKLIPNTNYCVSVYLEHSDQAVIKSPKCTLLP 205
DB 71 VPSSSL-----GTQFYICN-----VNHKPSMTKVDKVE----- 99
QY 206 PGQESSESASADKTHCPAPAPELLGSPVFLFPPKPKDTLMSKRPETVCVVVDVSH 265
DB 100 -----PKSCDKTHHTPCPAPAPELLGSPVFLFPPKPKDTLMSKRPETVCVVVDVSH 152
QY 266 DPEYKFNWYDGVENAHNAKTRPREQYNSTYRVYSVLTVLHODLNGEKCKYSNKA 325
DB 153 DPEYKFNWYDGVENAHNAKTRPREQYNSTYRVYSVLTVLHODLNGEKCKYSNKA 212
QY 326 APIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFPYSDIAVEMESNGOP 385
DB 213 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOP 272
QY 386 NYKTTTPVLDSDGSFLLYSKLTVDKSRWQGNVFNFSVMEHALNHNHTQKSLSP 443
DB 273 NYKTTTPVLDSDGSFLLYSKLTVDKSRWQGNVFNFSVMEHALNHNHTQKSLSP 330

RESULT 2
GC2_HUMAN STANDARD: PRT: 326 AA.
ID GC2_HUMAN
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG CAMMA-2 CHAIN C REGION.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82197621.
RA Ellison J.W., Hood L.E.;

RT "Linkage and sequence homology of two human immunoglobulin gamma
 heavy chain constant region genes.";
 Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 [12]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE: 81007673.
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications.";
 J. Immunol. 125:1048-1054(1980).
 [13]
 RN SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE: 80001357.
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein.";
 Can. J. Biochem. 57:758-767(1979).
 [14]
 RN SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE: 80114419.
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulin gamma chains.";
 Mol. Immunol. 16:923-925(1979).
 [15]
 RN REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RT Submitted (MAR-1980) to the PIR data bank.
 [16]
 RN SEQUENCE OF 1-121 (DOT).
 RX MEDLINE: 95255298.
 RA Scoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";
 Eur. J. Biochem. 228:886-893(1995).
 [17]
 RN DISULFIDE BONDS.
 RX MEDLINE: 72033500.
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 Biochem. J. 121:217-225(1971).
 [18]
 RN DISULFIDE BONDS.
 RX MEDLINE: 69064124.
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 Nature 221:145-148(1969).
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 CC -----
 DR EMBL: V00554: CAA23814.1: -;
 DR EMBL: V00554: CAA23815.1: -;
 DR EMBL: V00554: CAA23816.1: -;
 DR EMBL: V00554: CAA23817.1: -;
 DR PIR: A02148: G2HU.
 DR MIM: 147110: -;
 DR INTERPRO: IPR000495: -;
 DR INTERPRO: IPR003006: -;
 DR PIRAM: PF00067: Ig, 3.
 DR PROSITE: PS00290: IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 83
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 246 304
 FT VARIANT 60 60
 FT SITE 156 156 S -> A (IN MYELOMA PROTEINS TIL & ZIE).
 FT MOD_RES 326 326 /FTID-VAR_003889.
 FT SEQUENCE 326 AA; 35864 MW; 8310878C687BCF9C CRC64;
 SO
 Query Match 48.8% Score 1160; DB 1; Length 326;
 Best local similarity 69.2%; Pred. No. 1-3e-75;
 Matches 222; Conservative 21; Mismatches 26; Indels 52; Gaps 5;
 QY 128 PPSIVEEELQPLSLVIEQSEGIVKHKHPETKMGSGNFTYITDKLIPNPNVCSVY-- 185
 Db 53 FPAYLQSSGLYSLSVY-----TVPSSNFGQTGTC 83
 QY 186 -LEHSDEQAVIKSP--KCTLLPQGESESAESADKHTTCCPCAPPELLGGSVFLPFPK 242
 Db 84 NVDRKPSNTWKVKDYERKCV-----ECPPCPAP--VAGPSVFLPFPK 125
 QY 243 PKDTLMISRTPEVTCVVDVSHEDPEVKFNMYDQVEYHNKTREROYSTVYVSVL 302
 Db 126 PKDTLMISRTPEVTCVVDVSHEDPEVQFNMYDQVEYHNKTREROYSTVYVSVL 185
 QY 303 TVLHODWLNKGRKYCKVSNKALPAPTEKTSKAKQPREPOVYTLPPREKTKNQVSLT 362
 Db 186 TVVHODWLNKGRKYCKVSNKALPAPTEKTSKAKQPREPOVYTLPPREKTKNQVSLT 245
 QY 363 CLVKGFTPSDIAVWESNGQPENNKTTTPVLDSDGSFFLYSKLTVDRKSRMQGNVFS 422
 Db 246 CLVKGFTPSDIAVWESNGQPENNKTTTPVLDSDGSFFLYSKLTVDRKSRMQGNVFS 305
 QY 423 VMHEALNHNYTKSLSPGK 443
 Db 306 VMHEALNHNYTKSLSPGK 326
 RESULT 3
 GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-4 CHAIN C REGION.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1.11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE: 70207560.
 RA Ploek J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 RT constant region of a gamma 4 chain.";
 RL Biochem. J. 117:33-47(1970).
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DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 19; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin C region; Glycoprotein; Transmembrane;
 KW Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match
 Best Local Similarity 36.1%; Score 857; DB 1; Length 329;
 Matches 168; Conservative 46; Mismatches 65; Indels 38; Gaps 6;

OY 151 IYKHKPE---IGN-----MSGNFTYIIDKLIPNTNYCVSYLHSDQ 192
 DB 27 LVKGYPEPVYKWMNGALSSGVTVSSVLSGFSLSLVTPSSTW-----PSQ 77
 OY 193 AVIKSPKCTILPPGOESSEASAD---KTHICP--PCPAPELLGSPVFLPPPKDT 246
 DB 78 TVI-----CNVAHPASKTELIRIKRIEPIRIPKSTPPGSSCPGNIILGSPVFIIPPKDA 132
 OY 247 LMISRTPEVTCVVDVSHDEPEYKFMVYDGEVHNNAKTRPREOYNSTYRVSVLTVLH 306
 DB 133 LMISLTPKTYTCVVDVSEDDPDVHVSFVNDKEVHTAMQPREAOYNSTFRVVSALPIQH 192
 OY 307 OQMLNGEKYCKVSNKALPAPIETISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVK 366
 DB 193 QDMNRKKEKCKVNNKALPAPIETISKPKRQTPQVYTIIPPRQMSKKKSLTCLVT 252
 OY 367 GFYPSDIAVWESNGCPENNYKTPPVLDSDGSFLYSKLTVDKSRMOCGNFSCVMHE 426
 DB 253 NFPESEASIVEMERNGLEDYKNTPEILDSDGTFFLYSKLTVDTSMLGELFTCSVHE 312
 OY 427 ALHNHYTOKSLSLSPGK 443
 DB 313 ALHNHHTOKNLRSRPGK 329

RESULT 9
 GC3M_MOUSE
 ID GC3M_MOUSE STANDARD: PRT: 398 AA.
 AC P03987;
 DT 23-OCT-1986 (rel. 02, Created)
 DT 01-AUG-1991 (rel. 19, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85027161.
 RA Weis J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blatner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene.";
 RL EMBO J. 3:2041-2046(1984).
 RN [2]
 RP SEQUENCE OF 328-398 FROM N.A.
 RX MEDLINE: 84041483.
 RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
 RA Wall R.;
 RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
 RT segment.";
 RT Nucleic Acids Res. 11:6775-6785(1983).
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DR EMBL: J00451; AAB59655.1; -
 DR EMBL: V01526; CAA24767.1; ALT_SEQ.
 DR PIR: A02155; G3MSM.
 DR INTERPRO: IPR000495; -
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 19; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 FT DOMAIN 346 362 POTENTIAL.
 FT TRANSMEM 363 398 CYTOPLASMIC (POTENTIAL).
 FT CONFLICT 333 333 E -> G (IN REF. 2).
 FT CONFLICT 342 342 E -> Q (IN REF. 2).
 FT CONFLICT 388 388 P -> F (IN REF. 2).
 SQ SEQUENCE 398 AA; 43929 MW; CFT7264B50A4B95 CRC64;

Query Match
 Best Local Similarity 35.6%; Score 846; DB 1; Length 398;
 Matches 166; Conservative 46; Mismatches 65; Indels 38; Gaps 6;

OY 151 IYKHKPE---IGN-----MSGNFTYIIDKLIPNTNYCVSYLHSDQ 192
 DB 27 LVKGYPEPVYKWMNGALSSGVTVSSVLSGFSLSLVTPSSTW-----PSQ 77
 OY 193 AVIKSPKCTILPPGOESSEASAD---KTHICP--PCPAPELLGSPVFLPPPKDT 246
 DB 78 TVI-----CNVAHPASKTELIRIKRIEPIRIPKSTPPGSSCPGNIILGSPVFIIPPKDA 132
 OY 247 LMISRTPEVTCVVDVSHDEPEYKFMVYDGEVHNNAKTRPREOYNSTYRVSVLTVLH 306
 DB 133 LMISLTPKTYTCVVDVSEDDPDVHVSFVNDKEVHTAMQPREAOYNSTFRVVSALPIQH 192
 OY 307 OQMLNGEKYCKVSNKALPAPIETISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVK 366
 DB 193 QDMNRKKEKCKVNNKALPAPIETISKPKRQTPQVYTIIPPRQMSKKKSLTCLVT 252
 OY 367 GFYPSDIAVWESNGCPENNYKTPPVLDSDGSFLYSKLTVDKSRMOCGNFSCVMHE 426
 DB 253 NFPESEASIVEMERNGLEDYKNTPEILDSDGTFFLYSKLTVDTSMLGELFTCSVHE 312
 OY 427 ALHNHYTOKSLSLSP 441
 DB 313 ALHNHHTOKNLRSRPGK 327

RESULT 10
 GCB_RAT
 ID GCB_RAT STANDARD: PRT: 333 AA.
 AC P20761;
 DT 01-FEB-1991 (rel. 17, Created)
 DT 01-FEB-1991 (rel. 17, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE IG GAMMA-2B CHAIN C REGION.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89232738.
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 DR PIR: PS0018; PS0018.

RESULT	11			
ID	GCL_RAT	STANDARD;	PRT;	326 AA.
AC	P20739;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-FEB-1999 (Rel. 38, Last annotation update)			
DE	IG GAMMA-1 CHAIN C REGION.			
OS	Rattus norvegicus (Rat).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 89232738.			
RA	Brueggemann M.;			
RT	"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";			
RL	Gene 74:473-482(1988).			
DR	PIR: PS0017; PS0011.			
DR	INTERPRO: IPR000495; -.			
DR	INTERPRO: IPR003006; -.			
DR	PFAM: PF00047; Ig 3.			
DR	PROSITE: PS00290; IG_MHC; 1.			
KW	Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.			
FT	NON_TER	1	1	
FT	DOMAIN	1	97	CH1.
FT	DOMAIN	98	112	HINGE.
FT	DOMAIN	113	219	CH2.
FT	DOMAIN	220	326	CH3.
FT	DISULFID	27	82	
FT	DISULFID	102	102	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	106	106	INTERCHAIN (WITH A HEAVY CHAIN).

RESULT	12
GC1_MOUSE	
ID	GC1_MOUSE
AC	P01868
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DE	30-MAY-2000 (Rel. 39, Last annotation update)
OC	IG GAMMA-1 CHAIN C REGION.
CC	Mus musculus (Mouse).
CC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RP	[1]
RX	SEQUENCE FROM N.A.
RX	MEDLINE: 80045036.
RA	Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA	Takahashi N., Mano Y.;
RT	"Cloning and complete nucleotide sequence of mouse immunoglobulin
RT	gamma 1 chain gene.";
RL	Cell 18:559-568(1979).
RN	[2]
RP	SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX	MEDLINE: 80202559.
RA	Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA	Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT	"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT	cloned in a bacterial plasmid.";
RL	Gene 9:87-97(1980).
RN	[3]
RP	SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX	MEDLINE: 80012837.
RA	Rogers J., Clarke P., Salsler W.;
RT	"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT	heavy chain.";
RL	Nucleic Acids Res. 6:3305-3321(1979).
RN	[4]
RP	SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX	MEDLINE: 78242288.
RA	Adetugbo K.;
RT	"Evolution of immunoglobulin subclasses. Primary structure of a
RT	murine myeloma gammal chain.";


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DB      314 LHHHTOKLRSRPGK 329

RESULT 14
GC1M_MOUSE      STANDARD:      PRT:      393 AA.
AC      P01869;
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-AUG-1991 (Rel. 19, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 80045036.
RA      Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA      Takahashi N., Mano Y.;
RT      "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT      gamma 1 chain gene.";
RL      Cell 18:559-568(1979).
RN      [2]
RP      SEQUENCE OF 323-393 FROM N.A.
RX      MEDLINE; 82197626.
RA      Tyler B.M., Coman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT      "mRNA for surface immunoglobulin gamma chains encodes a highly
RT      conserved transmembrane sequence and a 28-residue intracellular
RT      domain.";
RL      Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN      [3]
RP      SEQUENCE OF 323-366 FROM N.A.
RX      MEDLINE; 82115295.
RA      Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA      Eisenberg D., Wall R.;
RT      "Gene segments encoding transmembrane carboxyl termini of
RT      immunoglobulin gamma chains.";
RL      Cell 26:19-27(1981).
RN      [4]
RP      SEQUENCE OF 1-44 FROM N.A.
RX      MEDLINE; 82222190.
RA      Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT      "Nucleotide sequences of gene segments encoding membrane domains of
RT      immunoglobulin gamma chains.";
RL      Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC      -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC      SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC      GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC      BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC      IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC      SEGMENT OF MU CHAINS.
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; V00793; CAA24172.1; -
DR      EMBL; V00793; CAA24173.1; -
DR      EMBL; V00793; CAA24174.1; -
DR      PIR; B02159; G1MSM
DR      MGI; 96446; IGH-4.
DR      INTERPRO; IPR000495; -
DR      INTERPRO; IPR003006; -
DR      PFAM; PF00047; Ig_3.
DR      PROSITE; PS00290; IG_MHC; 1.
KM      Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW      Alternative splicing; Transmembrane.
FT      NON_TER      1

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FT      DOMAIN      1      97
FT      DOMAIN      98      110
FT      DOMAIN      111      217
FT      DOMAIN      218      324
FT      DISULFID      27      82
FT      DISULFID      102      102
FT      DISULFID      104      104
FT      DISULFID      107      107
FT      DISULFID      109      109
FT      DISULFID      138      138
FT      CARBOHYD      174      174
FT      DISULFID      244      302
FT      TRANSMEM      340      357
FT      DOMAIN      358      393
SQ      SEQUENCE      393 AA; 43386 MM; 40C88343B7A1CE27 CNG64;

Query Match      34.5%; Score 820.5; DB 1; Length 393;
Best Local Similarity      56.4%; Pred. No. 2,3e-51;
Matches 150; Conservative 45; Mismatches 52; Indels 19; Gaps 5;

OY      189 SDEQAVIKSP-----LKTILPFGGSESASADKTH-----CPP--CPABELIGFSV 236
DB      65 SSVTVPSPPSPSEETVTCNVAHPA-----STPKVDKKIIPRDGCKPCICTVPEV---SSV 117
OY      237 FLFPPKPKDTLIMISRPETVCVVVDSHEDPEVKFNMYVDGVEVNAKTKPREQYNSTY 296
DB      118 FIFPKPKPDVLITITTPRYTCVYVISKDDPEVQSMFVDDVEVHTAOTQPREQFNSTF 177
OY      297 RVYSVLTVLHODMLNGEKYCKSKVSKALPAPLEKTISSAKGQPREQVYTTLPSPREEMTK 356
DB      178 RVSSELPIMHODPWLNGKREKFCVNSAAPPAPLEKTISSKGRKAPQYTTLPPEQMAK 237
OY      357 NOVSTLCYKGYPSDIAVEMESNQENNYKTPPYLDSGGSFELYKLYDKSRWQG 416
DB      238 DKVSLTCMHTDFEPDITVEWQMGPAENYKNTQPMNTNGSYFVKLVQKSNMEAG 297
OY      417 NVFSCSVNHEALNHNHYTOKSLSLSPG 442
DB      298 NTFCTSVLHEGLHNHTEKSLSHSPG 323

RESULT 15
GCAA_MOUSE      STANDARD:      PRT:      330 AA.
ID      GCAA_MOUSE
AC      P01863;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      IG GAMMA-2A CHAIN C REGION, A ALLELE.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 81076554.
RA      Sikorav J.-L., Auffray C., Rougeon F.;
RT      "Structure of the constant and 3' untranslated regions of the murine
RT      Balb/c gamma 2a heavy chain messenger RNA.";
RL      Nucleic Acids Res. 8:3143-3155(1980).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 81198976.
RA      Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT      "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT      and evolution of heavy chain genes: further evidence for intervening
RT      sequence-mediated domain transfer.";
RL      Nucleic Acids Res. 9:1365-1381(1981).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 81223894.
RA      Olio R., Auffray C., Mochamps C., Rougeon F.;
RT      "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes

```

Job time: 188 sec

```
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE; 74175517.
RA Bourgois A.; Fougereau M.; Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE; 73056887.
RA de Preval C.; Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
CC -----
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CC -----
CC EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR INTERPRO; IPR000495; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; I9; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KM Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 34.3%; Score 816; DB 1; Length 330;
Best Local Similarity 60.0%; Pred. No. 3.7e-51;
Matches 153; Conservative 31; Mismatches 57; Indels 14; Gaps 3;

QY 199 LKCTLLPQGESSESASADK-----THTCPP--CPAPELGSPVFLPPPKKDTLM 248
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 80 ITCVNAHPA-----SSTVVDKKIEPRGPTIKPCPRCKCPAPNLGSPVFIFFPKIKDYL 135
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 249 ISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTRPREEQYNSTYRVVSVLTVLIHQD 308
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 136 ISLSPIVTCVVVDVSEDDPQVQISMFVNNVEVHTAQOTHREDYNSLTIRVYSALPIQHOD 195
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 309 WLNGKEKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGF 368
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 196 WMSGKEPKCKVNNKDLPAPIERTISKPRGSRAPOVYVLPPEPEEMTKKQVTLTCMYTDF 255
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 369 YPSDIAEVEMSNQGPENNYKTTTPVLDSGSEFFLYSKLTVDKSRMOOGNVCSCVMHEAL 428
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 256 MPEDIIYEWNTNNGTELTNKTPEVLDSGSYFMYSKLRVEKKNWVERNSYSCSVVHGL 315
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 429 HNHYTOKSLSLSPGK 443
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 316 HNHHTTKSFSRTPGK 330
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: December 14, 2000, 10:30:40

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 14, 2000, 10:26:47 ; Search time 27.57 Seconds
(without alignments)
1019.691 Million cell updates/sec

Title: US-09-166-298-26

Perfect score: 2377

Sequence: 1 ISYSPDYTDESCFTKSLR.....MHEALHNHYTQKSLSLSPGK 443

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-65:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	124.4	52.3	330	1 GHHR	Ig gamma-1 chain C
2	124.2	52.3	374	2 SG9339	Ig heavy chain V r
3	123.8	52.1	374	2 S72664	Ig heavy chain V r
4	123.5	52.0	255	4 S31866	Ig gamma-1 chain C
5	1183.5	49.8	377	2 A23511	Ig gamma-3 chain C
6	1181.5	49.7	377	2 A60764	Ig gamma-3 chain C
7	1179	49.6	234	2 PT0207	Ig gamma chain C r
8	1160	48.8	326	1 G2HU	Ig gamma-2 chain C
9	1153.5	48.5	327	1 G4HU	Ig gamma-2 chain C
10	114.8	48.3	289	1 G3HOMI	Ig gamma-3 heavy c
11	114.4	48.1	331	2 A54295	Ig gamma-1 chain/b
12	114.4	48.1	331	2 S59501	interferon alpha/b
13	114.4	48.1	515	2 S59502	interferon recepto
14	114.0	48.0	515	2 I39073	interferon alpha-b
15	932.5	39.2	323	1 GHRB	Ig gamma chain C r
16	911	38.3	328	2 I47159	Ig gamma 2a chain
17	911	38.3	328	2 I47159	Ig gamma 2a chain
18	904	38.0	277	2 I47152	Ig gamma 4 chain c
19	890	37.4	328	2 I47158	Ig gamma 1 chain c
20	888.5	37.4	329	1 G2CP	Ig gamma-2 chain c
21	881	37.1	328	2 I47161	Ig gamma 3 chain c
22	866.5	36.5	470	2 S22080	Ig heavy chain pre
23	858.5	36.1	308	2 C30554	Ig heavy chain C r
24	858.5	36.1	472	2 S31459	Ig gamma-1 chain -
25	857	36.1	329	1 G3MSC	Ig gamma-3 chain C
26	846	35.6	398	1 G3MSM	Ig gamma-2 chain C
27	842.5	35.4	333	2 PS0018	Ig gamma-2b chain
28	834	35.1	444	2 PC4436	Ig gamma-1 chain C
29	826	34.7	326	2 PS0017	Ig gamma-1 chain C

30	825.5	34.7	324	1 G1MS	Ig gamma-1 chain C
31	822.5	34.6	329	2 S00847	Ig gamma-2c chain
32	820.5	34.5	393	1 G1MSM	Ig gamma-1 chain C
33	816	34.3	330	1 G2MSA	Ig gamma-2a chain
34	816	34.3	469	2 S37483	Ig gamma-2a chain
35	811	34.1	335	1 G2MSAB	Ig gamma-2a chain
36	811	34.1	399	1 G2MSAM	Ig gamma-2a chain
37	802	33.7	322	2 PS0019	Ig gamma-2a chain
38	801	33.7	446	2 S40295	Ig gamma-2b chain
39	793.5	33.4	474	2 S25057	Ig gamma-2b chain
40	786	33.1	336	1 G2MS11	Ig gamma-2b chain
41	781	32.9	405	1 G2MSB	Ig gamma-2b chain
42	770.5	32.4	327	2 S06611	Ig gamma-2 chain C
43	766	32.2	475	2 S01321	Ig gamma heavy cha
44	708	29.8	180	2 I46732	Ig gamma heavy cha
45	583.5	24.5	249	2 S69340	Ig heavy chain VHI

ALIGNMENTS

RESULT 1
GHHR
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence.revision 18-Aug-1982 #text.change 16-Jul-1999
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker
A:Note: Lys-330 is removed after translation
R:Harits, L.J.
Submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takehashi, N.; Ueda, S.; Obata, M.; Nikaide, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Maxdal, M.J.; Edelman
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A:Reference number: A90563; MUID:71064024
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-135 <CUN>
A:Note: this sequence has the G1m(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Het
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1

1gen Primerstruktur.
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein N1e
A:Accession: B91668
A:Molecule type: Protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A:Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hopppe-Seyley's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: Protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'W', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A:Note: This sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dieler, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hopppe-Seyley's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
A:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Exons: 99/1, 114/1, 224/1
A:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into Ia
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:247-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: Interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: Interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match	Similarity	Score	DB 1:	Length	330:
Best Local	Similarity	68.7%	Pred. No.	3.9e-80;	
Matches	246;	Conservative	19;	Mismatches	45; Indels 48; Gaps 6;
QY	88	SCNTTFLFCSHNMWLAIDMSFEP--PEFEIAGFTNHINWAKFPSEIVEEELDFSLDVLVE	145		
Db	19	SGGTALAGC-----LVKDYFPEPTVSMNSGALISGVIT---FPAVLDSGLISLSSVYT	70		
Y	146	EOSEGIYVKKHKKPEIKGNMGSNFYIIDLKLPNTMYCVSVYLEHSDQAVIKSPKCTLLP	205		
Db	71	VYSSSL-----GTQFYICN-----VNHKPSNTRKYDKKVE-----	99		
QY	206	PGQESASASADKTHNCPAPAPELLGGSPSYFLRPPKPKDILMSTRPEVTCVYVDVSH	265		
Db	100	-----PKSCDTHNCPAPAPELLGGSPSYFLRPPKPKDILMSTRPEVTCVYVDVSH	152		
QY	266	DEYVENWYVDGVEVHNNAKTRPREQYNSTYRVVSVLVLELQDMVLNGREYKCKVSNKALP	325		
Db	153	DEYVENWYVDGVEVHNNAKTRPREQYNSTYRVVSVLVLELQDMVLNGREYKCKVSNKALP	212		
QY	326	APIEKTISAKGQPREQVYTLPPSRREEMTKNQVSLTCLVKGFTPSDIAVEMESNGQPE	385		
Db	213	APIEKTISAKGQPREQVYTLPPSRREEMTKNQVSLTCLVKGFTPSDIAVEMESNGQPE	272		
QY	386	NKTTTPPVLDSDSFFLYSKLTVDKSRMOQGNVSCSYMHALLNHNHYOKSLSTSPGK	443		
Db	273	NKTTTPPVLDSDSFFLYSKLTVDKSRMOQGNVSCSYMHALLNHNHYOKSLSTSPGK	330		

RESULT	2	
1g heavy chain V region precursor - human		
569339		
C:Species: Homo sapiens (man)		
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000		
R:Khamilich, A.A.; Auconturier, P.; Preud'homme, J.L.; Cogne, M.		
Eur. J. Biochem. 229, 54-60, 1995		
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition dist		
A:Reference number: 569339; MUID:95262687		
A:Accession: 569339		
A:Status: preliminary		
A:Molecule type: mRNA		
A:Residues: 1-374 <KHA>		
A:Cross-references: EMBL:X81695		
C:Superfamily: immunoglobulin C region; immunoglobulin homology		
Query Match	52.3%;	Score 1242; DB 2; Length 374;
Best Local Similarity	78.9%;	Pred. No. 6.3e-80;
Matches 243; Conservative 10; Mismatches 27; Indels 28; Gaps 5;		
QY 153 KKHKEIKGNM-----SGNFTY----IDKLIPTMNYC-YSV-----YLEHSDQAVI 195		
DB 78 KRYSFLKRLRLITTDTSKNQVYLMTNVADPADVTATYICGISVEBQIGGQIRHNSGQGLT 137		
QY 196 KSPLEKCTLLPGQSESAESADKTHTCPCPAPELLGGPSVLFPPKPKDTLMISRTPEV 255		
DB 138 VT-----VSSEPKSCDKHTCCPCPAPELLGGPSVLFPPKPKDTLMISRTPEV 186		
QY 256 TCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKRREQVYNSTRYVSVLTLYLHODMLNGKEY 315		
DB 187 TCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKRREQVYNSTRYVSVLTLYLHODMLNGKEY 246		
QY 316 KCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREREKTNQVSLTCLVKGFYPSDIAV 375		
DB 247 KCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREREKTNQVSLTCLVKGFYPSDIAV 306		
QY 376 EWESNGQPENNKQTPPYLDSGSEFELYSKLTVDKSRMQGVFCSVHREALHNNHYTOK 435		
DB 307 EWESNGQPENNKQTPPYLDSGSEFELYSKLTVDKSRMQGVFCSVHREALHNNHYTOK 366		
QY 436 SLTSLSPGK 443		
DB 367 SLTSLSPGK 374		
RESULT 3		
S72664		
1g heavy chain V region precursor - human		
C:Species: Homo sapiens (man)		
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000		
R:Khamilich, A.A.		
submitted to the EMBL Data Library, September 1994		
A:Reference number: S72664		
A:Accession: S72664		
A:Status: preliminary		
A:Molecule type: mRNA		
A:Residues: 1-374 <KHA>		
A:Cross-references: EMBL:X81695		
C:Superfamily: immunoglobulin C region; immunoglobulin homology		
Query Match	52.1%;	Score 1238; DB 2; Length 374;
Best Local Similarity	99.1%;	Pred. No. 1.2e-79;
Matches 228; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
QY 214 ESADKTHHCPCPAPELLGGPSVLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 273		
DB 145 KSCDKTHHCPCPAPELLGGPSVLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 204		


```
Db 186 TVVHODMLNGEKYCKVSNKGLPAPRIEKTISKTKGQPEPEQVYTLPPSRREMTKNQVSLT 245
QY 363 CLVAGFPSPDIWVESNGQPENNYKTPPVLDSDGSFELYSKLTVDKSRMOQGNVSCS 422
Db 246 CLVAGFPSPDIWVESNGQPENNYKTPPVLDSDGSFELYSKLTVDKSRMOQGNVSCS 305
QY 423 VMHEALHNHYTKSLSLSPGK 443
Db 306 VMHEALHNHYTKSLSLSPGK 326

RESULT 9
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A>Note: The sequence was determined from the germ-line gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant r
A:Reference number: A90249; MUID:70207360
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30; 81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Intons: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa)
hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 16
C:Superfamily: immunoglobulin C region; immunoglobulin C region; immunoglobulin
C:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: Interchain (to light chain) #status experimental
F:21-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: Interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 48.5%: Score 1153.5; DB 1: Length 327;
Best Local Similarity 70.3%: Pred. No. 8,6e-74;
Matches 222; Conservative 19; Mismatches 34; Indels 41; Gaps 3;

QY 128 FPSIVEEELQFDLSVTEEGSEGVKKHKPRKMGNSFNFIIDKLIPNTNVCVSYLE 187
Db 53 FPAVLQSSGLXLSISVTVPSSSL-----GRTKTYTN-----VD 86
QY 188 HSDEQAVIKSPKCTLLPQOESSESASADKTHCPCPAPELLGGSVLEFPKPKDTL 247
Db 87 HKPSNTKVDKRDVESKGRP-----CPCSPAPELLGGSVLEFPKPKDTL 131
QY 248 MISTPPEVTCVVYVSHEDPEVKKNWYDGVENNAKTGREEDYNSTRVSVLTVLHQ 307
Db 132 MISTPPEVTCVVYVSHEDPEVKKNWYDGVENNAKTGREEDYNSTRVSVLTVLHQ 191
QY 308 DWLNGEKYCKVSNKGLPAPRIEKTISKTKGQPEPEQVYTLPPSRREMTKNQVSLT 367
Db 192 DWLNGEKYCKVSNKGLPAPRIEKTISKTKGQPEPEQVYTLPPSRREMTKNQVSLT 251
QY 368 FVPSDIWVESNGQPENNYKTPPVLDSDGSFELYSKLTVDKSRMOQGNVSCSVMHEA 427
```

```
Db 252 FVPSDIWVESNGQPENNYKTPPVLDSDGSFELYSKLTVDKSRMOQGNVSCSVMHEA 311
QY 428 LHNHYTKSLSLSPGK 443
Db 312 LHNHYTKSLSLSPGK 327

RESULT 10
G3HUVI
Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A90198; A93915; A02149
R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea
A:Reference number: A90442; MUID:81021548
A:Contents: heavy chain disease protein Wls
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <FRA>
A>Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A>Note: this protein lacks most of the V region and all of the CH1 region. Residue 12
R:Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicat
A:Reference number: A92219; MUID:77118561
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protel
A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MIC>
A>Note: the hinge region in gamma-3 chains is about four times as long as in other ga
idue segment (12-28)
A>Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in
R:Mollenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of t
A:Reference number: A90198; MUID:77021516
A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residu
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125/'EB',128-226,228-289 <MOU>
A>Note: this protein lacks most of the V region, all of the CH1 region, and part of t
R:Alexander, A.; Steinmetz, M.; Barilla, D.; Frangione, B.; Franklin, E.C.; Hood,
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deleti
A:Reference number: A93915; MUID:82247835
A:Contents: heavy chain disease protein Omn
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70;72-114,116-125,'E',127-133,'L',135-136,'E',138,'V',140-154,'D',156-
A>Note: a carboxyl-terminal Lys is removed posttranslationally
A>Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein Wls is shown.
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyrogutamic acid
F:203-270/Domain: immunoglobulin homology <IM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 48.3%: Score 1148; DB 1: Length 289;
Best Local Similarity 86.1%: Pred. No. 1,8e-73;
Matches 211; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 198 PLKCTLLPQOESSESASADKTHCPCPAPELLGGSVLEFPKPKDTLMISTPPEVTC 257
```

```
Db 45 PKSCDTPPCPCPCPCPCDTPPCPCPCAPBELLGGBSVFLFPKPKDILMISRTPEVTC 104
Oy 258 VVVDVSHEDPEVKNMYVDGVEVHNAKTRPREOYNSTYRVSVLTVLEHODWLNKEYKC 317
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 105 VVVVDVSHEDPEVGFKNMYVDGVEVHNAKTRPREOYNSTYRVSVLTVLEHODWLNKEYKC 164
Oy 318 KYSNKAALPAPIETKISKAGOPREPOVYTLPPSREKTKNOVSLTCLYKGFYSDIAVEW 377
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 165 KYSNKAALPAPIETKISKAGOPREPOVYTLPPSREKTKNOVSLTCLYKGFYSDIAVEW 224
Oy 378 ESNGOPENNYKTPPVILDSGSEFFLYSKLTVDSKRMQOQNVFSCSVMEHALHMYTQKSL 437
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 225 ESSGOPENNYNTTPPMLDSGSEFFLYSKLTVDSKRMQOQNVFSCSVMEHALHMYTQKSL 284
Oy 438 SLSPG 442
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 285 SLSPG 289

RESULT 11
A54295
Interferon alpha/beta receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999
C:Accession: A54295
R:Novick, D.; Cohen, B.; Rubinstein, M.
Cell 77, 391-400, 1994
A:Title: The human interferon alpha/beta receptor: characterization and molecular cloning
A:Reference number: A54295, MUID:94236684
A:Accession: A54295
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-331 <NOV>
A:Cross-references: GB:X77722; NID:q488363; PIDN:CA054785.1; PID:q488364
C:Keywords: cytokine receptor

Query Match 48.1%; Score 1144; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.1e-73;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ISYDSPDYDESCFTFKISLNFNRSILSMELKNHSIYPTHTLLYTIMSKPEDLKVVKNCA 60
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 27 ISYDSPDYDESCFTFKISLNFNRSILSMELKNHSIYPTHTLLYTIMSKPEDLKVVKNCA 86
Oy 61 NTRRSFCDLTDEMRSTHEAVTVLEGFSGNTLFFSCSHNFWLAIDMSFEPPEEIVGFTN 120
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 87 NTRRSFCDLTDEMRSTHEAVTVLEGFSGNTLFFSCSHNFWLAIDMSFEPPEEIVGFTN 146
Oy 121 HINWVKFPSIVEEELQFDLSLVIEOSEGIVKHKPEIKGNMSGNTYIIDKLIPNTNY 180
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 147 HINWVKFPSIVEEELQFDLSLVIEOSEGIVKHKPEIKGNMSGNTYIIDKLIPNTNY 206
Oy 181 CVSYLEHSDQAVIKSPLKCTLLPQGESESAESA 216
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 207 CVSYLEHSDQAVIKSPLKCTLLPQGESESAESA 242

RESULT 12
S59501
Interferon receptor JFNAR 2-1 - human
C:Species: Homo sapiens (man)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S59501
R:Luttfalla, G.; Holland, S.J.; Cinato, E.; Monneron, D.; Reboul, J.; Rogers, N.C.; Smith
EMBO J. 14, 5100-5108, 1995
A:Title: Mutant USA cells are complemented by an interferon-alpha-beta receptor subunit
A:Reference number: S59501; MUID:96067138
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-331 <LUT>
C:Keywords: alternative splicing; cytokine receptor
```

```
Query Match 48.1%; Score 1144; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.1e-73;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ISYDSPDYDESCFTFKISLNFNRSILSMELKNHSIYPTHTLLYTIMSKPEDLKVVKNCA 60
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 27 ISYDSPDYDESCFTFKISLNFNRSILSMELKNHSIYPTHTLLYTIMSKPEDLKVVKNCA 86
Oy 61 NTRRSFCDLTDEMRSTHEAVTVLEGFSGNTLFFSCSHNFWLAIDMSFEPPEEIVGFTN 120
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 87 NTRRSFCDLTDEMRSTHEAVTVLEGFSGNTLFFSCSHNFWLAIDMSFEPPEEIVGFTN 146
Oy 121 HINWVKFPSIVEEELQFDLSLVIEOSEGIVKHKPEIKGNMSGNTYIIDKLIPNTNY 180
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 147 HINWVKFPSIVEEELQFDLSLVIEOSEGIVKHKPEIKGNMSGNTYIIDKLIPNTNY 206
Oy 181 CVSYLEHSDQAVIKSPLKCTLLPQGESESAESA 216
    VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Db 207 CVSYLEHSDQAVIKSPLKCTLLPQGESESAESA 242

RESULT 14
I39073
Interferon alpha-beta receptor, beta subunit long form - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C:Accession: I39073
R:Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.; Patha, P.; Colamo
J. Biol. Chem. 270, 21606-21611, 1995
A:Title: Cloning and expression of a long form of the beta subunit of the interferon
A:Reference number: I39073; MUID:95394915
A:Accession: I39073
A:Status: preliminary; translated from GB/EMBL/DBJ
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 14, 2000, 10:26:43 ; Search time 28.35 Seconds
(without alignments)
534.316 Million cell updates/sec

Title: US-09-166-298-26

Perfect score: 2377
Sequence: 1 ISYSPDYTDSCFTKISLR.....MHEALHNHYTKSLSPGK 443

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_36.*
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15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT.*
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21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1274.5	53.6	784	21	IL-13/IL-4 dual tr
2	1271	53.5	424	16	Human soluble kit
3	1270	53.4	424	16	Human soluble kit
4	1266.5	53.3	376	19	Antigenic peptide
5	1266	53.3	466	13	Sequence encoded b
6	1263	53.1	477	20	hB7.2Fc soluble fu
7	1262	53.1	454	14	H52H4-160 murine a
8	1258.5	52.9	437	18	Alpha-1-acid glyco
9	1256.5	52.9	475	17	Monoclonal antibod
10	1253.5	52.7	476	18	Primalised anti-hu
11	1253.5	52.7	476	19	Macaque primatized
12	1253	52.7	470	7	Chimeric human-mou

13	1253	52.7	470	8	P70547	Sequence of novel
14	1253	52.7	470	19	W83037	Anti-Fas humanised
15	1253	52.7	470	21	W90929	Humanised HFE7A de
16	1253	52.7	470	21	W90933	Humanised anti-Fas
17	1253	52.7	470	21	W90934	Humanised anti-Fas
18	1253	52.7	470	21	W90935	Humanised anti-Fas
19	1253	52.7	470	21	W90936	Humanised HFE7A de
20	1251.5	52.7	376	18	W50287	Human Fas antigen
21	1251.5	52.7	472	20	Y50157	Chimeric mouse/hum
22	1251	52.6	460	21	Y69890	Human NR6alpha/IgG
23	1251	52.6	963	19	W70540	Integrin beta-1 ch
24	1251	52.6	1367	19	W70542	Integrin alpha-2 c
25	1250	52.6	330	20	Y50153	Human heavy chain
26	1250	52.6	396	18	W18574	Aggrecanase artili
27	1250	52.6	396	18	W18575	Aggrecanase artili
28	1250	52.6	451	20	Y50031	Human E27 anti-19E
29	1250	52.6	451	20	W95659	Mus musculus anti-
30	1250	52.6	451	20	W95661	Mus musculus anti-
31	1250	52.6	451	20	W95663	Mus musculus anti-
32	1250	52.6	451	21	Y85201	Light chain amino
33	1250	52.6	452	20	Y29458	Recombinant immuno
34	1250	52.6	452	21	Y77766	Humanised anti-IL-
35	1250	52.6	453	14	R33311	Humanised MacELI Ve
36	1250	52.6	453	20	Y50151	Antibody P19 chime
37	1250	52.6	453	21	Y85199	Heavy chain amino
38	1250	52.6	476	19	W01822	Primalised anti-hu
39	1250	52.6	476	19	W63765	Macaque primatized
40	1250	52.6	690	21	Y92195	Human IL-6R-alpha-
41	1249	52.5	452	19	W69316	Anti-IL-8 humanise
42	1249	52.5	470	19	W83036	Anti-Fas humanised
43	1249	52.5	470	21	W90926	Humanised HFE7A de
44	1249	52.5	488	18	W08349	Eporec fusion prot
45	1248	52.5	449	14	R43339	Completely humanis

ALIGNMENTS

RESULT	1
Y92207	standard: Protein; 784 AA.
ID	Y92207
XX	AC Y92207;
XX	01-AUG-2000 (first entry)
DE	IL-13/IL-4 dual trap, IL-4R-alpha,IL-13R-alpha-1-Fc fusion protein.
XX	IL-13/IL-4 dual trap; cytokine; antagonist; CNTF; receptor;
KW	fusion protein; cytosstatic; immunomodulator; osteopathic.
XX	
OS	Synthetic.
XX	Homo sapiens.
XX	
FT	Key
FT	Protein
FT	Location/Qualifiers
FT	1..231
FT	/label= "human,IL-4-R-alpha
FT	/note= "extracellular domain"
FT	232..233
FT	/label= linker
FT	234..555
FT	/label= IL-13-R-alpha-1
FT	/note= "extracellular domain"
FT	556..557
FT	/label= linker
FT	558..784
FT	/label= human_Fc
PN	W0200018932-A2.
XX	
PD	06-APR-2000.
XX	
PF	22-SEP-1999; 99WO-US22045.

Qy	42	LYIYIMSKPEDL---	KVKNKCANTTRSFCDLJDEMRSTHEAYVTVLEFGSGNFTLFESC	98
Db	17	llfnplvktegiicrnrvtlnvkdvcklvanlpkd-----	ymtllyvpgmdvlp	66
Qy	99	NFMFLA---IDMSFEPE---	FELV--GFMNHINVMKPFPSIYEEELQPLSLVIEQSE	149
Db	67	hcvlsemvngvdsdltldlckfnsiseglsny-slicklvynd---	divecvknss	120
Qy	150	GIYKK--HKPEIKGMSGNFTYIIDKL-----	PNTNYC--SVYLEHSDQAVIK	166
Db	121	klklksfksperrllfpbeeffrlfnrldafkdvfaselsdcvssatl	epkdsrsvl	186
Qy	197	SPLKCTLLPQGOSESASDKTTCPCPCAPELLGGPSFLFPPKCDLMTSRPEVT	256	
Db	181	kpf---mlppraadpepksckltlccppcapelll99psvlllppkpkdlmstrpevt	237	
Qy	257	CVVVVDSHEDPEYKFMNVYDGEVYHNKTKPREROYNSTRVYSVLVTLHODMLNGKEYK	316	
Db	238	cvvvvdshepexkfmnydgvvevhnaktprceegynslyrvsvlvtlvhqdwingeyk	297	
Qy	317	CKVSNKALLPAPIETIKSKAGOPREPOVYTLPLPSREEMTKNOVSLTGLVNGFYPSDLAVE	376	
Db	298	ckvsnakllpapieltkstkayqprepvuytlpsrdeitknqysltclvnygfypsdlave	357	
Qy	377	WESNGQENNYKTTTPVYLDSDGSEFELSKTLVDKSRMOQGNVFCSCVMHALLNHYTKS	436	
Db	358	wesngqennyktttppvlyldsdgsfellyskltlvdkstrvgqgnvlfscsvmhallnhytkfs	417	
Qy	437	LSLSPEK	443	
Db	418	lslspek	424	

RESULT	3
ID	W14764
AC	W14764 standard; Protein; 424 AA.
XX	
DT	11-JUN-1997 (first entry)
DE	Human soluble kit ligand-IgG fusion protein.
XX	
KW	kit ligand; c-kit proto-oncogene; cytokine; growth factor; hematopoietic cell; cell proliferation; stem cell; anaemia; thrombocytopenia; therapy; IgG1.
OS	Homo sapiens.
FH	Key
FT	Peptide
FT	/label= Sig_peptide 1..25
FT	/note= "KL signal peptide"
FT	Protein
FT	26..424
FT	/label= Mat_protein
FT	/note= "human KL-IgG fusion"
XX	
PN	WO9526199-A1.
PD	05-OCT-1995.
XX	
PF	28-MAR-1995; 95WO-US03866.
XX	
PR	28-MAR-1994; 94US-0220379.
XX	
PA	(CYTO-) CYTOMED INC.
PI	Lobell RB, Nocka KH;
DR	WPI; 1995-351198/45.
DR	N-PSDB; T63109.
XX	
TX	Covalent dimers of kit ligand or FLT-3/FLK-2 ligand - exhibit

PT increased activity in promoting cell proliferation
XX
XX
PS Claim 10; Page 43-44; 88pp; English.
XX
XX A fusion protein (W14764) between human soluble kit ligand (KL)
CC (see also W14761) and a human IgG1 heavy chain can be transiently
CC expressed in COS cells transfected with a human KL-Ig cDNA
CC construct (T63109) in vector CDM8; a corrected KL-Ig construct
CC (W14765) has also been prep'd. KL-Ig can also be produced as a
CC dimer stabilised by intermolecular disulphide bonds or a peptide
CC linker. The stabilised KL-Ig dimers have a more favorable cell
CC proliferation: mast cell activation ratio than native KL and can
CC stimulate haematopoietic recovery or stem cell/progenitor cell
XX mobilisation with less toxicity.
XX
XX Sequence 424 AA;

Query Match	53.48;	Score 1270;	DB 16;	Length 424;
Best Local Similarly	62.58;	Pred. No. 2e-85;		
Matches 267;	Conservative 37;	Mismatches 79;	Indels 44;	Gaps 12;

QY	42	LLYITMSKPEBL----	KVKKNCANTTRSPCDLTDEMRSTHEAIVTVLEGESEGNTTLPSCSH	98
Db	17	llfplrvktegicnrvtnnnkdvtklvanlpkd-----	ymcltkyvgmdllps---	66
QY	99	NFWLA---IDMSFEPPE----	FELIV--GFMNHIVMWKPPSIVEEELQPLSLVIEQOSE	149
Db	67	hcwlsenmvgvqidsdltldldfsmlesglsoy-sllcklvanlv-----	divecvvsnss	120
QY	150	GIYVK--HKPEIKGNMGSNFTYIIIDKLI-----	PNTNYGCV--SVYLEHSDGQAVIK	196
Db	121	kdlkksfksperrllfcpbeeffrlfnrsldatklfdvasetsdcvvasatl	spexdsrvsvl	180
QY	197	SPLKCTLLPQGEESMSASDKTTCPCPCAPPELLGGPSVFLPPRKKOTLMSIRPEVT	256	
Db	181	kp f---mlpvaadpepkscktlctppcapelll99psvllfpbkpckdlmstrpevt	237	
QY	257	CVVVYDVSHEDPEVFMNYVDGVEVHNKTRPREEOYSTRVVSVLVLLHQDMLNGKEY	316	
Db	238	cvvvdvshedpevfkfmnyvdgvevhnaktprreegyngsvlrvsvlvtlvlnqwdlnqdeyk	297	
QY	317	CKVSNKALPAIETITISKAGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFPSPDIAYE	376	
Db	298	ckvsnkalpapietiktiskagqprepvuytlppsrdeitknqvsiltclvkgfypsdlave	357	
QY	377	MESNGQNNNNKTRPPVLDSDGSFELYSKTLVDRSRMOQGNVFSCSGMHAIINHTQKS	436	
Db	358	wesngqnnnnktrppvldsdgsfilylskltvdksrtvgqgnvfscsmhealnnhytqks	417	
QY	437	LSLSPGK	443	
Db	418	lslspgk	424	

RESULT	4
ID	W60037 standard; Protein; 376 AA.
XX	
AC	W60037;
XX	
DT	11-SEP-1998 (first entry)
XX	
DE	Antigenic peptide hFas (nd29) containing Fc region.
XX	
KW	Fas ligand; Fas antagonist; apoptosis related disease; liver disease;
KW	heart failure; kidney failure; graft-versus-host disease; antibody;
XX	myocardial infarction; ischemic restenosis; endotoxic shock.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
Peptide	1-16
FT	

```

FT      Protein                               /note= "hFas antigen signal peptide"
FT      30..376
XX      /note= "hFas (nd29) protein"
XX      MO9818487-A1.
XX      07-MAY-1998.
XX      31-OCT-1997; 97MO-JP03978.
XX      26-SEP-1997; 97JP-0262521.
XX      31-OCT-1996; 96JP-0290459.
XX      27-DEC-1996; 96JP-0351718.
XX      (MOCH ) MOCHIDA PHARM CO LTD.
XX      (OSAB-) OSAKA BIOSCIENCE INST.
XX      Nagata S, Suda T, Vatoml T;
XX      WPI; 1998-271925/24.
XX      N-PSDB; V34430.
XX      Use of Fas antagonist for treatment and prevention of
XX      apoptosis-related diseases - such as heart or kidney failure,
XX      graft-versus-host disease or liver disease
XX      Examples: Fig 5-9; 86pp; Japanese.
XX      This represents the antigenic peptide hFas (nd29) containing the FC
XX      region. The invention provides the use of Fas antagonist as an agent for
XX      the treatment and prevention of apoptosis-related diseases. The Fas
XX      antagonist can be a partial Fas antigen peptide containing the
XX      extracellular part of the protein, but lacking the signal sequence, an
XX      anti-Fas antibody, or an anti-Fas ligand antibody, where the antibody is
XX      preferably a humanized antibody. The Fas antagonist is used in the
XX      treatment and prevention of diseases such as myocardial infarction, heart
XX      failure, ischemic heart disease, acute kidney failure, graft-versus-host
XX      disease, ischemic restenosis of the heart, liver or kidney, and
XX      endotoxic shock, and also as an organ preservative in transplantation.
XX      The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
XX      system.
XX      Sequence 376 AA:
SQ
Query Match 53.3%; Score 1266.5; DB 19; Length 376;
Best Local Similarity 86.4%; Pred. No. 3.1e-85;
Matches 241; Conservative 6; Mismatches 17; Indels 15; Gaps 4;
OY 176 PNTNYCVSVYLEHSD-----EQAVIKSLPKCTLL-----PPQSESESASADKTHTCPP 224
    || : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 102 pnf-fcnsfvcchodpctckehglik---ecllsnkckkeegsrnsrpsckdthtcpp 157
OY 225 CPAPELLIGGSVFLFPKPKDYLIMISTPREVCYVVDVSHEDPEVKFNMTYDGVHNNAK 284
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 158 cpapelllggsvflfpkpkdylimistprevcyvvvdshdpevkfnmyvdgvevnmak 217
OY 285 TKREBOYNSTYRVSVLTWLDHMDLNGKEYKCKVSNKALPAPKEKTSIRAKGQRPBPYV 344
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 218 tkpreegynstlyrvsvltwldhmdlmgkeykckvsnkalpaplektlsrakgqprepyv 277
OY 345 YTLPPSHEEMTKNOVSLTCLVKGFPYSDIAVEMWESNGCPENNYKTPPVLDSDGFFLYS 404
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 278 ytlpperdeltknqvsltcvkgfypsdiavevewesngqpennykttppvldsdgsfflys 337
OY 405 KLVVDKSRMOOGQVNFSCSVNHEALHNHTOKSLSLSPGK 443
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 338 klvvdksrvmogqvnfscsvnmhealhnhtqslslspgk 376
XX
RESULT 5
R24812
ID R24812 standard; Protein; 466 AA.

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```

XX      AC R24812;
XX      DT 28-DEC-1992 (first entry)
XX      DE Sequence encoded by the chimeric H chain cDNA contained in pTB1373.
XX      KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;
XX      KM antithrombotic agent; myocardial infarction therapy.
XX      OS Synthetic.
XX      FH Key Location/Qualifiers
XX      FT Peptide 13..19
XX      FT 20..134 /label= Leader
XX      FT Region /label= VH
XX      FT Region 135..232 /label= CH1
XX      FT Region 233..247 /label= hinge
XX      FT Region 248..357 /label= CH2
XX      FT Region 358..464 /label= CH3
XX      FT Misc-difference 465
XX      FT /note= "translated stop codon"
XX      PN EP491351-A.
XX      PD 24-JUN-1992.
XX      PF 17-DEC-1991; 91EP-0121591.
XX      PR 18-DEC-1990; 90JP-0413829.
XX      PR 11-NOV-1991; 91JP-0294464.
XX      PA (TAKE ) TAKEDA CHEM IND LTD.
XX      PI Iwasa S, Taka H, Watanabe T, Tada H;
XX      DR WPI; 1992-209528/26.
XX      DR N-PSDB; Q25692.
XX      PT Chimeric monoclonal antibodies - contain anti-human fibrin
XX      PT antibody light and heavy chain variable and constant for treating
XX      PT thrombotic conditions e.g. myocardial infarction
XX      PS Example: Figure 11; 87pp; English.
XX      CC Plasmid pTB1373 contains the whole length of a mouse-human
XX      CC chimeric anti-human fibrin heavy chain cDNA open reading
XX      CC frame. It was prep'd using Poly(A)+ RNA from the anti-fibrin
XX      CC chimeric Ab-producing transforment FIB1-HO1/63 as a template
XX      CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
XX      CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH
XX      CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
XX      CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
XX      CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
XX      CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'C1H
XX      CC respectively as a primer for first strand cDNA synthesis and the
XX      CC 5'SH and 3'UH respectively as primers for PCR. The amplified gene
XX      CC products were isolated and used to produce plasmids. After
XX      CC confirmation of the cDNA sequence of each plasmid, the cDNA
XX      CC encoding LH, VH, CH1 and CH2CH3 were joined together to give
XX      CC plasmid pTB1373 contg. the whole length chimeric H chain
XX      CC (LH, VH, CH1, CH2CH3), also abbreviated as 19H-FIB,
XX      SQ Sequence 466 AA:
Query Match 53.3%; Score 1266; DB 13; Length 466;

```

Best Local Similarity 59.4%; Pred. No. 4.4e-85;
Matches 274; Conservative 23; Mismatches 80; Indels 84; Gaps 13;

OY 1 ISVDSPTYDESC--TFKISLRNFRSLTSMELKNHSIVPTHTLLTYTMSKPEDLKAVKN 58
Db 70 ISVGTGLYPSDMKGRIFSLIDNARILYIQL---SSLSRDLTAMY-----Y 113
OY 59 CANTRSFCDLTDEM-----RSTHEAVYTVL---EGFSGNTTLFSCSHNFWLAI 104
Db 114 CGN-----fademdywgqglvtvssastkqpsvfrlpsskstggtcaalgc-----lvk 164
OY 105 DMSERP--PEFEIVGFTNHINWVKFPSIVEELQFDLSLIVIEQSGICVKKHPEIKGN 162
Db 165 dyfepvtswnsgaltsghlt---fpavlsqslslyssvvtvpsasl----- 210
OY 163 MSGFTYIIDLINNTNVCVSVLEHSDQAVIKSPIKCTLLPPGQSESAESADKPTTC 222
Db 211 -gltqlyl-----ct---vnhkpsntkvdkrve-----pkscdktltc 243
OY 223 PCPCAPELLGSPVFLPPPKRDTLMTSRPEVTQVVDVSHEDPEVKNFYVDGVEYHN 282
Db 244 ppcpapellgspvflfrppkrdtltmstrpevtcvvdvshedpevkfmyvgdvevhn 303
OY 283 AKTKPREBQYNSTYRVVSVLTVLHQDWLNGEKYCKVSNKALPAPIEKTISKAGQPREP 342
Db 304 aktkpreeqynstlyrvsvltvlhqdwlngkyckvsnkalpapielktlakagqprep 363
OY 343 QVYTLPPSRREMTKNQVSLTCLVKGFPSTDAVEMESGQENNYKTPRPVLDSDGFRFL 402
Db 364 qvyltlppsrreemtknqvsiltclvkgfypsdlavewesngqenmykltprvldsdgsfll 423
OY 403 YSKLTVDKSRWQGNVFCSVYHAEALHNHYTKSLSPK 443
Db 424 yskltvdksrtwgqgnvfscsymhealhnhytkslspsk 464

RESULT 6
ID W90207 standard; Protein; 477 AA.
XX
AC W90207;
XX
DT 10-MAY-1999 (first entry)
XX
DE hb7.2Fc soluble fusion protein.
XX
KM B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
KM CD86; T cell activation; inhibitor; graft versus host disease;
KM transplant rejection; allograft rejection; autoimmune disease;
KM allergy; therapy; human; antibody; hb7.1Fc.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
FX Key Location/Qualifiers
FT Peptide 1..16
FT /note= "potential eukaryotic secretory signal
FT /note= "peptide"
FT Domain 17..239
FT /note= "human B7.2 (mature protein) extracellular
FT /note= "human B7.2 domain"
FT Peptide 240..245
FT /note= "introduced by PCR cloning strategy"
FT Protein 246..477
FT /note= "human IgG1-Fc (hinge-CH2-CH3)"
XX
XX WO9858965-A2.
XX
XX 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-EP03791.
XX
XX 20-JUN-1997; 97EP-0870092.

XX
PA (INNO-) INNOGENETICS NV.
XX
PI Bosman A, Buysse M, Lorie K, Sablon E;
XX
DR WPI; 1999-105615/09.
XX
PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection
XX
PS Example 3.1.1.3; Fig 3; 182pp; English.
XX
CC This 54 kDa soluble fusion protein, termed hb7.2Fc, is composed of
CC human co-stimulatory molecule B7.2 extracellular domain fused
CC C-terminally to human IgG1-Fc. It was produced by PCR
CC amplification of hb7.2 cDNA in plasmid pcDNAneo/hb7.2, and
CC insertion of the amplified cDNA into pVL-Fc (ICCG3048), resulting
CC in pVLshb7.2-Fc (ICCG3004) baculovirus transfer plasmid. The invention
CC relates to molecules such as diabodies, trivalent and tetraivalent
CC antibodies and small antigen binding peptides which can cross-link,
CC or cross-react with, B7.1 and B7.2 expressed on professional
CC antigen presenting cells leading to the inhibition of
CC antigen-specific T cell activation. Methods to produce such
CC molecules are provided. The molecules are used to treat or prevent
CC diseases of the immune system, in particular graft rejection, graft
CC versus host disease, allergy and autoimmune diseases (claimed).
XX
SO Sequence 477 AA;
Query Match 53.1%; Score 1263; DB 20; Length 477;
Best Local Similarity 69.2%; Pred. No. 7.4e-85;
Matches 252; Conservative 34; Mismatches 52; Indels 26; Gaps 8;
OY 99 NFWLAIDMSFEPPEP-ETVGFTHINWVKFPSIVEELQFDLSLIVIEQS-----EGIV 152
Db 121 nselvianfsgpeltvpsnltenvylnltcsslmgypkkmvllrtkntslieygdgm 180
OY 153 KKHNP-----EIKGMSGNFTYIIDLIPNTNVCVSVLEHSDQAVIKRPLAKTL--- 203
Db 181 qksqdnvtefydvsilsvsfvdvtsnm--tlfcl--le-tktrllsspfstledp 233
OY 204 -LPPGOES---ESASADKTHTCPCPCAPELLGSPVFLPPPKRDTLMTSRPEVTQV 259
Db 234 qppdhnspqldqpsckdktltcpcpapellgspvflfrppkrdtltmstrpevtcv 293
OY 260 VDVSHEDPEVKFNMYVDGVEYHNAKTKPREBQYNSTYRVVSVLTVLHQDWLNGEKYCKV 319
Db 294 vdvshedpevkfnmyvdgvevhnaktkpreeqynstlyrvsvltvlhqdwlngkyckv 353
OY 320 SNKALPAPIEKTISKAGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFPSTDAVEMES 379
Db 354 snkalpapielktiskagqprepyvltlpsrdeltkqvsltlcvxgfydsdlavewes 413
OY 380 NGQENNYKTPRPVLDSDGSEFLYSKLTVDKSRWQGNVFCSVYHAEALHNHYTKSL 439
Db 414 ngqennmyktrprvldsdgsfllyskltvdksrtwgqgnvfscsymhealhnhytksls 473
OY 440 SPGK 443
Db 474 spgk 477

RESULT 7
ID R30774 standard; protein; 454 AA.
XX
AC R30774;
XX
DT 12-MAY-1993 (first entry)
XX
XX H52H4-160 murine anti-CD18 antibody heavy chain.
XX

XX	Humanisation; rapid; monoclonal antibody.
XX	
OS	Mus musculus.
XX	
PN	MO9222653-A.
XX	
XX	23-DEC-1992.
PD	
XX	
PF	15-JUN-1992; 92MO-US05126.
XX	
PR	14-JUN-1991; 91US-0715272.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Carter PJ, Presta LG;
XX	
DR	WPI; 1993-018139/02.
PT	
XX	
PT	Humanisation of antibodies - by molecular modelling of the variable
XX	domains and alteration by gene conversion mutagenesis
PS	
XX	Disclosure; Fig 6A; 126pp; English.
XX	
CC	The sequence is that of the heavy chain of murine anti-CD18
CC	antibody H52H4-160.
XX	
XX	
XX	
Sequence	454 AA;

XX	W10552;
AC	
XX	
DT	22-APR-1997 (first entry)
XX	
DE	Alpha-1-acid glycoprotein-IgG1 fusion protein.
XX	
KM	IgG1; alpha-1-acid glycoprotein; AGP; sialyl-Lewis X;
KW	inflammation; extravasation-dependent adverse reaction;
KM	organ damage; clotting; adult respiratory distress syndrome;
KW	glomerular nephritis; ischemic myocardial injury; immune reaction;
KM	septic shock; septicaemia; therapy; diagnosis.
XX	
OS	Homo sapiens.
XX	
PN	W09700079-A1.
XX	
PD	03-JAN-1997.
XX	
PF	11-JUN-1996; 96MO-US10043.
XX	
PR	14-JUN-1995; 95US-0000213.
XX	
PA	(GEHO) GEN HOSPITAL CORP.
XX	
PI	Pouyan T, Seed B;
XX	
DR	WPI; 1997-077356/07.
DR	N-PSDB; T60740.
XX	
PT	P-selectin and opt. E-selectin binding organic mol. - having
PT	sialyl-Le(x) and sulphated determinant, useful for protecting
XX	against inflammatory or immune reactions
PS	
XX	Disclosure; Page 44-45; 81pp; English.
CC	
CC	A fusion protein (W10552) is composed of human acute phase
CC	alpha-1-acid glycoprotein (AGP) and the constant domains of human
CC	IgG1. It is expressed in host cells utilizing a DNA construct
CC	(T60740) obtd. by inserting alpha-1-AGP cDNA into an expression
CC	cassette contd. the IgG1 hinge-CH2-CH3 sequences. sialyl-Le(x)
CC	addition sites may be introduced into the antibody fusion protein
CC	e.g. by appending a P-selectin ligand (see also W10530-32). The
CC	sialyl-Le(x) sites interfere with the antibody's ability to fix
CC	complement or bind an Fc receptor. Expression in
CC	fucosyltransferase-expressing host cells allows prodn. of soluble
CC	antibody fusion proteins. These have therapeutic applns., e.g. in
CC	minimising inflammation and decreasing extravasation-dependent
CC	organ damage and/or clotting.
XX	
50	Sequence 437 AA;

0Y	221	TCPCPCAEELLGGSPVFLFPKPKDTLMTISTPTECTCVVVDVSHEDPEVKFMWYVDGVEV	280
Db	215	tcpcpcapelllgpsvflfppkpkdtlmtistpctcvvdvshedpevktmwyvdgvev	274
0Y	281	HNAKTKPREEOYNSTRVAVSVLTVLVHODMLNGKEKCKVSNKALPAPLEKTSKAKGQPR	340
Db	275	hnaktkpreegynstrvavsvlvtlhqdwlngkeykckvsnkalpapektskxkgqr	334
0Y	341	EPQVYTLPPSRREEMTKNOVSLTCLWKGGYPSDIAEWESNGCPENNRYTTPPVLDSDGSF	400
Db	335	epqvytlpdsrdeitlknqvsiltclvkgfypsdiawesngqpennrytctppvldsdgsf	394
0Y	401	FLYSKLTVDKSRMOGNYFSCSVMEALHNHYTOKSLSLSPGK	443
Db	395	flyskltvdksrwtggnvfscsvmhealhnhytqkslslspgk	437
RESULT	9		
ID	R93553		
XX	AC	R93553 standard; Protein: 475 AA.	
XX	R93553;		
DT	20-AUG-1996	(first entry)	
XX	XX		
DE	Monoclonal antibody DNA heavy chain against 65 kd hCMV antigen.		
XX	XX		
KW	Polymerase chain reaction; primer: amplify; PCR: light chain; Mab;		
KW	65 kd antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.		
XX	XX		
OS	Synthetic.		
XX	XX		
EH	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT	Protein	/note= "Signal peptide"	
FT		20..475	
FT		/note= "Mature heavy chain"	
XX	XX		
PN	JP08038178-A.		
XX	XX		
PD	13-FEB-1996.		
XX	XX		
PE	20-FEB-1995;	95JP-0030742.	
XX	XX		
PR	18-FEB-1994;	94JP-0021628.	
XX	XX		
PA	(NLSN) NISSHINBO IND INC.		
PA	(TANAKA/) TANAKA H.		
XX	XX		
DR	WPI: 1996-154852/16.		
DR	N-PSDB; T18059.		
XX	XX		
PT	Human monoclonal antibody binds to cytomegalovirus 65 kd antigen -		
PT	produced by primer amplification, used in the diagnosis of hCMV		
PT	infection		
XX	XX		
PS	Claim 4; Page 16-18; 22pp; Japanese.		
XX	XX		
CC	The sequences given in R93553-54 represent the heavy and light chains		
CC	respectively of a monoclonal antibody against a 65 kd antigen of human		
CC	cytomegalovirus (hCMV). The DNA's encoding these sequences were		
CC	amplified using the sequences given in T18040-58. The monoclonal		
CC	antibody may be used in the diagnosis of hCMV.		
XX	XX		
XX	Sequence 475 AA;		

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Query Match          52.9%  Score 1256.5;  DB 17;  Length 475;
Best Local Similarity 56.8%  Pred. No. 2.2e+84;
Matches 262;  Conservative 32;  Mismatches 92;  Indels 75;  Gaps 8;

QY      1 ISYDSDYTDDECTKRISLRNFRSLTSMELKMHSLVPHYLLTYLTKMSPK----- 51
      | | : | : : : : | : | | : | : | : | : | : | : | : | : | : | :

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Db	72	lyysstcltynpslksrvtlsvdaenngfslslssvlaadavvycatlsptgydllygsf	131
Qy	52	-----DLKVVKNCANTRTSFCDLTDWMSTHEAVYVLEGFSGNTLTFSCSHNFWLAT	104
Db	132	psywgqglvtlvsasatkgpsvflpapskst-----sgytaalg-----lvk	175
Qy	105	DMSFEP--PEEPIVQFTNHINMMKFPSPVIEDELOFDLSLVEEQSGIKKHNPELIGN	165
Db	176	dyfpepvtvswngaltsgvht---fpravlqssgllysllsvlvpsssl-----	221
Qy	163	MSGNTFYIIDLKLPNTNCVSVYLEHSDQAVIKSPKLCITLLPPGQESSESASADKTHTC	222
Db	222	-----gtctylcn-----vnhkpsnklvdkve-----pkscdkthtc	254
Qy	223	PPCPAPELLGGPSYFLFPKPKRDTLMTSRTEVTCVVVDVSHEDPEVKFNNYVDSGEVHN	282
Db	255	ppcpapelllgpsvslfppkpkdtlmslartpctvcvvvdvshedpevkfnnvdygevh	314
Qy	283	AKTRREGQYNSTRVNVSVLVLYHODMLNGEKYCKSKYSNKLPRLEKTIISKAKGQREP	342
Db	315	aktkpreeqnystlyvsvlrvlbnqdwlngkeyckvksnknlparlektliskakgqrep	374
Qy	343	QVYTLPPSREEMTKQVSLTCLVKGFEYSPSDIAVEMESNGQENNYKTHPPRLVDSGSFLL	402
Db	375	qvyltlppsrdelctknqvsiltclvkgfypsdlavewesngqennykthlpprlvdsdgsfl	434
Qy	403	YSKLTVDKSRMOQGNVFCSGYVMEALAHNHYYQKSLSLSPCK	443
Db	435	yskltvdksrwyggnvfscsymhealhhnhytqkslsisprk	475
RESULT	10		
ID	W01818	W01818 standard; Protein; 476 AA.	
XX	AC	W01818;	
XX	DT	25-MAY-1997 (first entry)	
XX	DE	Primatised anti-human B7.1 antigen antibody 7C10 heavy chain.	
XX	KM	Monoclonal antibody; cynomolgus monkey; macaque; 7C10;	
XX	KW	Primatised antibody; B7 antigen; CD28; Immunosuppressive;	
XX	KM	autoimmune disease; idiopathic thrombocytopenia purpura;	
XX	KW	systemic lupus erythematosus; rheumatoid arthritis; psoriasis;	
XX	KM	type 1 diabetes mellitus; graft versus host disease;	
XX	XX	hetero-hybridoma; transfectiona.	
OS	OS	Chimeric Macaca cynomolgus;	
OS	XX	Chimeric Homo sapiens.	
XX	PN	W09640878-A1.	
XX	PD	19-DEC-1996.	
PF	PF	06-JUN-1996; 96WO-US10053.	
PR	PR	07-JUN-1995; 95US-0487550.	
XX	PA	(IDEC-) IDEC PHARM CORP.	
XX	PI	Anderson DR, Breams P, Hanna N, Shestowsky WS;	
XX	DR	WPI; 1997-108638/10.	
XX	DR	N-PSDB; T62510.	
PT	PT	Monkey monoclonal antibody binding human B7.1 or B7.2 antigen	
PS	PS	useful for treating autoimmune disease or graft-versus-host disease	
CC	CC	Claim 6; Fig 8B; 81pp; English.	
CC	CC	2 Polypeptides (W01817 and W01818) respectively comprise primatised	
CC	CC	forms of the light and heavy chains of cynomolgus monkey anti-human	

PT money monoclonal antibody binding human B-1.1 Or B-1.2 antigen
XX useful for treating autoimmune disease or graft-versus-host disease
PS
XX
XX Claim 6; Fig 8B; 81pp; English.

CC 2 polypeptides (W01817 and W01818) respectively comprise primatised
CC forms of the light and heavy chains of cynomolgus monkey anti-human

[illegible]

ID	Sequence	Score	DB	Length	Query Match
Db 442	ggnvfscsymhealnhnlytqkslsipgk 470				
RESULT 13					
P70547					
P70547	standard; protein; 470 AA.				
AC	P70547;				
XX					
XX					
DF	12-FEB-1991 (first entry)				
XX					
DE	Sequence of novel mouse-human chimeric antibody H chain.				
XX					
KW	Leukaemia lymphoma diagnosis; tumour diagnosis;				
XX					
XX	novel mouse-human chimeric antibody H chain.				
OS	Homo sapiens and Mus musculus.				
XX					
FH	Key	Location/Qualifiers			
FT	Region	1..140			
FT		/note="Mouse V region"			
FT	Region	141..480			
FT		/note="Human C region"			
PN	JP62201598-A.				
XX					
PD	05-SEP-1987.				
XX					
PF	28-FEB-1986; 86JP-0041983.				
XX					
PR	28-FEB-1986; 86JP-0041983.				
XX					
PA	(TEIJ) TEIJTN KK.				
DR	WPI; 1987-288384/41.				
XX					
PT	Mouse-human chimera antibody H chain - comprises mouse antibody H				
PT	chain V region aminoacid sequence and human antibody C region				
XX	sequence, to react with leukaemia lymphoma antigen				
XX					
PS	Claim 8; Page 3; 21pp; Japanese.				
CC	A human gene library prepd. from isolated human chromosomal DNA, was				
CC	screened for human antibody H chain gene fragment contg. human				
CC	C-gamma-1 gene (see N70844, N70845, N70486 and N70882). A mouse				
CC	Nu-1 gene library prepd. from isolated mouse chromosomal DNA, was				
CC	screened for mouse antibody H chain gene; then the DNA sequence of				
CC	the VJ1 region of this gene was determined. Using the above human				
CC	and mouse genes, chimeric antibody gene expression vectors				
CC	pml-1, -2, -3, -4 and -5 were prepd.				
XX					
SO	Sequence 470 AA; -				
Query Match	52.7%; Score 1253; DB 8; Length 470;				
Best Local Similarity	66.1%; Pred. No. 3.9e-84;				
Matches 257; Conservative	22; Mismatches 48; Indels 62; Gaps				
88	SGNTTLFSCSH-NFMWLAIADMSFEPPEPEIIVGFTNHINV---MYKFPsIVEELQFDLSLV 1434				
Db	111 agtcttvtssygnltky-----fdwvgagtlvtvsaastkgspsv-----fplaps 154				
Qy	144 IEEOSEG-----IVKKHKPE---IKGMSGNFT-----YIIDKL--IPN 177				
Db	155 skstsgtaalgxixvkdyfpepvtvsw-n-sgaltsqyhtfpavilqssgylslssvltvs 213				
Qy	178 TNYCVSYVL---EHSDEGAVIKSPDKCTLPPEGESSASAEADKTHRCPCPCAPPELLGCP 234				
Db	214 sslgtqtqixlnvnhkpsntkvydkkve-----pscdktchcpcpapel119p 261				
Qy	235 SVFLPPPKPKDTLMI SRTPEVTCCVVVDVSHEDPEVKFNWVYDGEVNNATKPREEOYNS 294				
Db	262 svflfppkdkdtlmlsrtfpevtccvvvdvshbedpevkfnwvvdgevvnnatkpreeoyns 321				

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